

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2005, 18:07:03 ; Search time 139.455 Seconds
(without alignments)
981.776 Million cell updates/sec

Title: US-10-058-069-7
Perfect score: 1876
Sequence: 1 MGWSLILLFLVAVATRVLSQ.....MHEALHNYQKSLSLSPGK 354

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1876	100.0	354	AAE27926	Aae27926 Human CH2
2	1876	100.0	354	ABB82835	Abb82835 Antibody
3	1683	89.7	360	AAE27924	Aae27924 Human CH2
4	1683	89.7	360	ABB82833	Abb82833 Antibody
5	1614	86.0	470	AAE27923	Aae27923 Human C2B
6	1614	86.0	470	ABB82832	Abb82832 Antibody
7	1613.5	86.0	731	AAW52156	Aam52156 Humanised
8	1613.5	86.0	741	AAW52159	Aam52159 Humanised
9	1613	86.0	470	AAW52158	Aam52158 A dimeric
10	1608.5	85.7	729	AAW52157	Aam52157 Humanised
11	1608.5	85.7	739	AAW52161	Aam52161 Humanised
12	1603	85.4	470	AAW83036	Aaw83036 Anti-Fas
13	1603	85.4	470	AAW83036	Aaw83036 Anti-Fas
14	1603	85.4	470	AAW90926	Aaw90926 Humanised
15	1603	85.4	470	AAW90926	Aaw90926 Humanised
16	1603	85.4	470	AAW90926	Aaw90926 Humanised
17	1602.5	85.4	465	AAW90926	Aaw90926 Humanised
18	1602.5	85.4	465	AAW90926	Aaw90926 Humanised
19	1602.5	85.4	465	AAW90926	Aaw90926 Humanised
20	1595	85.0	470	AAW90933	Aaw90933 Humanised
21	1595	85.0	470	AAW90933	Aaw90933 Humanised
22	1593	84.9	470	AAW90934	Aaw90934 Humanised
23	1593	84.9	470	AAW90934	Aaw90934 Humanised
24	1592	84.9	470	AAW83037	Aaw83037 Anti-Fas
25	1592	84.9	470	AAW83037	Aaw83037 Anti-Fas

26	1592	84.9	470	3	AAW90935	Aaw90935 Humanised
27	1592	84.9	470	3	AAW90929	Aaw90929 Humanised
28	1592	84.9	470	5	ABB74944	Abb74944 Humanised
29	1592	84.9	470	5	ABB74898	Abb74898 Humanised
30	1592	84.9	470	5	ABB74904	Abb74904 Mouse hum
31	1579	84.2	470	3	AAW90936	Aaw90936 Humanised
32	1579	84.2	470	5	ABB74945	Abb74945 Humanised
33	1577.5	84.1	465	4	AAW72228	Aaw72228 Humanised
34	1573.5	83.9	464	8	ADJ11354	Adj11354 BHA10 V1#
35	1572.5	83.8	464	4	AAW72232	Aaw72232 Humanised
36	1565.5	83.4	467	6	ADA47341	Ada47341 TRX1 agly
37	1565.5	83.4	467	6	ADA47341	Ada47341 TRX1 agly
38	1565.5	83.4	467	6	ADA47336	Ada47336 TRX1 heavy
39	1565.5	83.4	467	6	ADA47342	Ada47342 TRX1 agly
40	1565.5	83.4	467	8	ADP88454	Adp88454 Antibody
41	1565.5	83.4	467	8	ADP88446	Adp88446 Antibody
42	1565.5	83.4	467	8	ADP88430	Adp88430 Antibody
43	1565.5	83.4	467	8	ADP88438	Adp88438 Antibody
44	1565.5	83.4	467	8	ADQ87966	Adq87966 Heavy cha
45	1565.5	83.4	467	8	ADQ87970	Adq87970 Heavy cha

ALIGNMENTS

RESULT 1
AAE27926
ID AAE27926 standard; protein; 354 AA.
AC AAE27926;
XX
XX
DT 27-DEC-2002 (first entry)
XX
DE Human CH2 domain deleted CC49 antibody heavy chain protein.
KW Human; CC49 antibody; C2B8 antibody; tumour associated antigen; TAG-72;
KW neoplasm; neoplastic disorder; haematologic neoplasm; colon cancer;
KW non-Hodgkin's lymphoma; haematologic malignancy; tumour.
XX
OS Homo sapiens.
PN WO200260955-A2.
XX
PD 08-AUG-2002.
XX
PF 29-JAN-2002; 2002WO-US002373.
XX
PR 29-JAN-2001; 2001US-0264318P.
PR 16-NOV-2001; 2001US-0331481P.
(IDEC-) IDEC PHARM CORP.
PI Braslawsky GR, Hanna N, Chinn P;
XX WPI; 2002-698547/75.
DR N-ESDB; AAD45755.
XX
PT Novel domain deleted CC49 antibody reactive with tumor associated antigen
XX -72, or C2B8 antibody reactive with CD20, useful for treating
XX myelosuppressed patient suffering from a neoplastic disorder.
XX
XX Example 2; Fig 4A; 74pp; English.

The present invention relates to domain deleted CC49 or C2B8 antibodies.
Domain deleted CC49 antibodies comprise a heavy chain human CC49 domain
deleted sequence in which CH2 domain has been deleted and are reactive
with tumour associated antigen (TAG)-72. The C2B8 antibodies are reactive
with CD20 and comprise a heavy chain having a sequence of a derived
domain deleted C2B8 construct where the CH2 domain has been deleted.
Sequences of the invention are useful for imaging a neoplasm. They are
also useful for treating myelosuppressed patients suffering from
neoplastic disorder such as haematologic neoplasm, preferably non-
Hodgkin's lymphoma. Antibodies of the invention are also used to treat

CC neoplastic disorder, colon cancer and haematologic malignancy. They are
 CC useful for reducing tumour size, inhibiting tumour growth and/or
 CC prolonging the survival time of tumour-bearing animals and for treating
 CC tumours. The present sequence is human CH2 domain deleted CC49 antibody
 CC heavy chain protein. This sequence is used in the exemplification of the
 CC invention
 XX
 SQ Sequence 354 AA;

Query Match 100.0%; Score 1876; DB 5; Length 354;
 Best Local Similarity 100.0%; Pred. No. 1.1e-114;
 Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGWSLILLFLVAVATRVLSQVQSGAEVVKPGASVKISCKASGYTFTDHAHIVKQNP 60
 DB 1 MGWSLILLFLVAVATRVLSQVQSGAEVVKPGASVKISCKASGYTFTDHAHIVKQNP 60
 QY 61 GQRLWIGYFSPGNDPFKYNRFKQKATLTADTSASTAYVELSLRSEDYAVYFCTRSLN 120
 DB 61 GQRLWIGYFSPGNDPFKYNRFKQKATLTADTSASTAYVELSLRSEDYAVYFCTRSLN 120
 QY 121 MAYWGQGLTVTVSSASTKGPSPVPLAPSSKTSSTGTAALGCLVKDYPEPVTVSWNSGAL 180
 DB 121 MAYWGQGLTVTVSSASTKGPSPVPLAPSSKTSSTGTAALGCLVKDYPEPVTVSWNSGAL 180
 QY 181 TSGVHTTTPAVLQSSGLYSLSVTVTPSSSLGTQYICNVNHPKSNVTVDKKEPKSCDKT 240
 DB 181 TSGVHTTTPAVLQSSGLYSLSVTVTPSSSLGTQYICNVNHPKSNVTVDKKEPKSCDKT 240
 QY 241 HTCPPCPGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKT 300
 DB 241 HTCPPCPGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKT 300
 QY 301 TTPVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 354
 DB 301 TTPVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 354

RESULT 2

ABB82835
 ID ABB82835 standard; protein; 354 AA.

XX AC ABB82835;

XX DT 31-MAR-2003 (first entry)

XX DE Antibody huCC49 CH2 domain deleted heavy chain.

XX CC49; antibody; cytostatic; antiallergic; antianemic; antiasthmatic;
 XX vsotropic; immunomodulator; protozoacide; antidiabetic; nephrotropic;
 XX thyromimetic; hepatotropic; haemostatic; antileprotic; antibacterial;
 XX neuroprotective; antiporiatic; antirheumatic; antiarthritic; antiulcer;
 XX dermatological; immunosuppressive; antiinflammatory.

XX OS Homo sapiens.

XX PN WO200296948-A2.

XX PD 05-DEC-2002.

XX PF 29-JAN-2002; 2002WO-US002374.

XX PR 29-JAN-2001; 2001US-0264318P.

XX PR 16-NOV-2001; 2001US-0331481P.

XX PR 21-DEC-2001; 2001US-0341858P.

XX FA (IDEC-) IDEC PHARM CORP.

XX PI Braslawsky GR, Hanna N, Chinn P, Hariharan K;

XX DR WPI; 2003-140446/13.

XX DR N-PSDB; ABZ24019.

XX XX

PT Novel dimeric antibody useful for treating immune disorder and neoplastic
 disorder, has several non-covalently associated monomeric subunits.

XX Example 1; Fig 4A; 78pp; English.

CC- The invention relates to a dimeric antibody (I) comprising several
 CC monomeric subunits, where the monomeric subunits are non-covalently
 CC associated. (I) is useful for treating a disorder, especially immune
 CC disorder, and neoplastic disorder such as relapsed Hodgkin's disease,
 CC resistant Hodgkin's disease high grade, low grade and intermediate grade
 CC non-Hodgkin's lymphomas, B cell chronic lymphocytic leukemia (B-CLL),
 CC lymphoplasmacytoid lymphoma (LPL), mantle cell lymphoma (MCL), follicular
 CC lymphoma (FL), diffuse large cell lymphoma (DLCL), Burkitt's lymphoma,
 CC AIDS-related lymphomas, monocytic B cell lymphoma, angioimmunoblastic
 CC lymphadenopathy, small lymphocytic, follicular, diffuse large cell,
 CC diffuse small cleaved cell, large cell immunoblastic lymphoblastoma,
 CC small, non-cleaved, Burkitt's and non-Burkitt's, follicular, mixed small
 CC cleaved and large cell lymphomas, in a mammal (see ABZ24017 for a
 CC detailed description of the various uses of (I)). The present sequence
 CC represents the antibody huCC49 CH2 domain deleted heavy chain

XX SQ Sequence 354 AA;

Query Match 100.0%; Score 1876; DB 6; Length 354;
 Best Local Similarity 100.0%; Pred. No. 1.1e-114;
 Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGWSLILLFLVAVATRVLSQVQSGAEVVKPGASVKISCKASGYTFTDHAHIVKQNP 60
 DB 1 MGWSLILLFLVAVATRVLSQVQSGAEVVKPGASVKISCKASGYTFTDHAHIVKQNP 60
 QY 61 GQRLWIGYFSPGNDPFKYNRFKQKATLTADTSASTAYVELSLRSEDYAVYFCTRSLN 120
 DB 61 GQRLWIGYFSPGNDPFKYNRFKQKATLTADTSASTAYVELSLRSEDYAVYFCTRSLN 120
 QY 121 MAYWGQGLTVTVSSASTKGPSPVPLAPSSKTSSTGTAALGCLVKDYPEPVTVSWNSGAL 180
 DB 121 MAYWGQGLTVTVSSASTKGPSPVPLAPSSKTSSTGTAALGCLVKDYPEPVTVSWNSGAL 180
 QY 181 TSGVHTTTPAVLQSSGLYSLSVTVTPSSSLGTQYICNVNHPKSNVTVDKKEPKSCDKT 240
 DB 181 TSGVHTTTPAVLQSSGLYSLSVTVTPSSSLGTQYICNVNHPKSNVTVDKKEPKSCDKT 240
 QY 241 HTCPPCPGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKT 300
 DB 241 HTCPPCPGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKT 300
 QY 301 TTPVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 354
 DB 301 TTPVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 354

RESULT 3

AAE27924
 ID AAE27924 standard; protein; 360 AA.

XX AC AAE27924;

XX DT 27-DEC-2002 (first entry)

XX DE Human CH2 domain deleted C2B8 protein.

XX KW Human; CC49 antibody; C2B8 antibody; tumour associated antigen; TAG-72;
 KW neoplasm; neoplastic disorder; haematologic neoplasm; colon cancer;
 KW non-Hodgkin's lymphoma; haematologic malignancy; tumour.

XX OS Homo sapiens.

XX PN WO200260955-A2.

XX PD 08-AUG-2002.

XX PF 29-JAN-2002; 2002WO-US002373.

XX 29-JAN-2001; 2001US-0264318P.
PR 16-NOV-2001; 2001US-0331481P.
XX (IDEC-) IDEC PHARM CORP.
XX Braslawsky GR, Hanna N, Chinn P;
XX WPI; 2002-698547/75.
DR N-PSDB; AAD45753.
XX Novel domain deleted C2B8 antibody reactive with tumor associated antigen
PT -72, or C2B8 antibody reactive with CD20, useful for treating
PT myelosuppressed patient suffering from a neoplastic disorder.
XX Example 1; Fig 1B; 74pp; English.
XX The present invention relates to domain deleted C2B8 or C2B8 antibodies.
CC Domain deleted C2B8 antibodies comprise a heavy chain human C2B8 domain
CC deleted sequence in which CH2 domain has been deleted and are reactive
CC with tumour associated antigen (TAG)-72. The C2B8 antibodies are reactive
CC with CD20 and comprise a heavy chain having a sequence of a derived
CC domain deleted C2B8 construct where the CH2 domain has been deleted.
CC Sequences of the invention are useful for imaging a neoplasm. They are
CC also useful for treating myelosuppressed patients suffering from
CC neoplastic disorder such as haematologic neoplasm, preferably non-
CC Hodgkin's lymphoma. Antibodies of the invention are also used to treat
CC neoplastic disorder, colon cancer and haematologic malignancy. They are
CC useful for reducing tumour size, inhibiting tumour growth and/or
CC prolonging the survival time of tumour-bearing animals and for treating
CC tumours. The present sequence is human CH2 domain deleted C2B8 protein.
CC This sequence is used in the exemplification of the invention
XX Sequence 360 AA;
SQ
Query Match 89.7%; Score 1683; DB 5; Length 360;
Best Local Similarity 88.6%; Pred. No. 4.5e-102;
Matches 319; Conservative 13; Mismatches 22; Indels 6; Gaps 1;
Qy 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTTTDAIHWVKQNP 60
Db 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTTTDAIHWVKQNP 60
Qy 61 GORLEWIGYFPGNDGDFKYNRFRKATLTADTASTAYVELSLRSDEDTAVYFCTRLN 120
Db 61 GORLEWIGYFPGNDGDFKYNRFRKATLTADTASTAYVELSLRSDEDTAVYFCTRLN 120
Qy 121 MA-----YMGOGTLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVS 174
Db 121 YGGDWYFNVWGAGTITVTSAASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVS 180
Qy 175 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKKVEP 234
Db 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKKVEP 240
Qy 235 KSCDKTHCTCPGCPGPPQVYTLPPSRDELTKNQVSLTCLVKGYFPPSDIAVEWESNGQP 294
Db 241 KSCDKTHCTCPGCPGPPQVYTLPPSRDELTKNQVSLTCLVKGYFPPSDIAVEWESNGQP 300
Qy 295 ENNYKTTTPVLDSGSLYSLTVDKSRWQGNVFCVSNVHEALHNNHTOKSLSLSPGK 354
Db 301 ENNYKTTTPVLDSGSLYSLTVDKSRWQGNVFCVSNVHEALHNNHTOKSLSLSPGK 360
RESULT 4
ABB82833
ID ABB82833 standard; protein; 360 AA.
XX AC ABB82833;
XX DT 31-MAR-2003 (first entry)
XX DE Antibody C2B8 CH2 domain deleted heavy chain.

XX C2B8; antibody; cytostatic; antiallergic; antianemic; antiasthmatic;
KW vsotropic; immunomodulator; protozoacide; antidiabetic; nephrotropic;
KW thyromimetic; hepatotropic; haemostatic; antileptotic; antibacterial;
KW neuroprotective; antipsoriatic; antirheumatic; antiarthritic; antiulcer;
KW dermatological; immunosuppressive; antiinflammatory.
XX Homo sapiens.
OS WO200296948-A2.
XX 05-DEC-2002.
XX 29-JAN-2002; 2002WO-US002374.
XX 29-JAN-2001; 2001US-0264318P.
PR 16-NOV-2001; 2001US-0331481P.
PR 21-DEC-2001; 2001US-0341858P.
XX (IDEC-) IDEC PHARM CORP.
XX Braslawsky GR, Hanna N, Chinn P, Hariharan K;
XX WPI; 2003-140446/13.
XX N-PSDB; ABZ24017.
XX Novel dimeric antibody useful for treating immune disorder and neoplastic
PT disorder, has several non-covalently associated monomeric subunits.
XX Example 1; Fig 1B; 78pp; English.
XX The invention relates to a dimeric antibody (I) comprising several
CC monomeric subunits, where the monomeric subunits are non-covalently
CC associated. (I) is useful for treating a disorder, especially immune
CC disorder, and neoplastic disorder such as relapsed Hodgkin's disease,
CC resistant Hodgkin's disease high grade, low grade and intermediate grade
CC non-Hodgkin's lymphomas, B cell chronic lymphocytic leukemia (B-CLL),
CC lymphoplasmacytoid lymphoma (LPL), mantle cell lymphoma (MCL), follicular
CC lymphoma (FL), diffuse large cell lymphoma (DLCL), Burkitt's lymphoma,
CC AIDS-related lymphomas, monocytic B cell lymphoma, angioimmunoblastic
CC lymphadenopathy, small lymphocytic, follicular, diffuse large cell,
CC diffuse small cleaved cell, large cell immunoblastic lymphoblastoma,
CC small, non-cleaved, Burkitt's and non-Burkitt's, follicular, mixed small
CC cleaved and large cell lymphomas, in a mammal (see ABZ24017 for a
CC detailed description of the various uses of (I)). The present sequence
CC represents the antibody C2B8 CH2 domain deleted heavy chain
XX Sequence 360 AA;
SQ
Query Match 89.7%; Score 1683; DB 6; Length 360;
Best Local Similarity 88.6%; Pred. No. 4.5e-102;
Matches 319; Conservative 13; Mismatches 22; Indels 6; Gaps 1;
Qy 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTTTDAIHWVKQNP 60
Db 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTTTDAIHWVKQNP 60
Qy 61 GORLEWIGYFPGNDGDFKYNRFRKATLTADTASTAYVELSLRSDEDTAVYFCTRLN 120
Db 61 GORLEWIGYFPGNDGDFKYNRFRKATLTADTASTAYVELSLRSDEDTAVYFCTRLN 120
Qy 121 MA-----YMGOGTLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVS 174
Db 121 YGGDWYFNVWGAGTITVTSAASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVS 180
Qy 175 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKKVEP 234
Db 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKKVEP 240
Qy 235 KSCDKTHCTCPGCPGPPQVYTLPPSRDELTKNQVSLTCLVKGYFPPSDIAVEWESNGQP 294
Db 241 KSCDKTHCTCPGCPGPPQVYTLPPSRDELTKNQVSLTCLVKGYFPPSDIAVEWESNGQP 300

Qy 295 ENNYKTPPPVLDSDGSPFLYKSLTVDKSRWQGNVFCSCVMHEALHNNHYTKQSLSPGK 354
 Db 301 ENNYKTPPPVLDSDGSPFLYKSLTVDKSRWQGNVFCSCVMHEALHNNHYTKQSLSPGK 360

RESULT 5
 ID AAE27923 standard; protein; 470 AA.
 AC AAE27923;
 XX
 DT 27-DEC-2002 (first entry)
 DE Human C2B8 antibody heavy chain protein.
 KW Human; C2B8 antibody; C2B8 antibody; tumour associated antigen; TAG-72;
 KW neoplasm; neoplastic disorder; haematologic neoplasm; colon cancer;
 KW non-Hodgkin's lymphoma; haematologic malignancy; tumour.
 XX
 OS Homo sapiens.
 PN WO200260955-A2.
 XX
 PD 08-AUG-2002.
 XX
 XX 29-JAN-2002; 2002WO-US002373.
 XX
 XX 29-JAN-2001; 2001US-0264318P.
 XX
 XX 16-NOV-2001; 2001US-0331481P.
 XX
 XX (IDEC-) IDEC PHARM CORP.
 FA
 XX
 XX Braslawsky GR, Hanna N, Chinn P;
 XX
 XX WPI; 2002-698547/75.
 XX N-PSDB; AAD45752.
 DR
 XX
 XX Novel domain deleted CC49 antibody reactive with tumor associated antigen
 PT -72, or C2B8 antibody reactive with CD20, useful for treating
 PT myelosuppressed patient suffering from a neoplastic disorder.
 XX
 XX Example 1; Fig 1A; 74pp; English.
 PS
 XX
 XX The present invention relates to domain deleted CC49 or C2B8 antibodies.
 CC Domain deleted CC49 antibodies comprise a heavy chain human CC49 domain
 CC deleted sequence in which CH2 domain has been deleted and are reactive
 CC with tumour associated antigen (TAG)-72. The C2B8 antibodies are reactive
 CC with CD20 and comprise a heavy chain having a sequence of a derived
 CC domain deleted C2B8 construct where the CH2 domain has been deleted.
 CC Sequences of the invention are useful for imaging a neoplasm. They are
 CC also useful for treating myelosuppressed patients suffering from
 CC neoplastic disorder such as haematologic neoplasm, preferably non-
 CC Hodgkin's lymphoma. Antibodies of the invention are also used to treat
 CC neoplastic disorder, colon cancer and haematologic malignancy. They are
 CC useful for reducing tumour size, inhibiting tumour growth and/or
 CC prolonging the survival time of tumour-bearing animals and for treating
 CC tumours. The present sequence is human C2B8 heavy chain protein. This
 CC sequence is used in the exemplification of the invention
 XX
 XX Sequence 470 AA;
 SQ

Query Match 86.0%; Score 1614; DB 5; Length 470;
 Best Local Similarity 67.7%; Pred. No. 2e-97;
 Matches 318; Conservative 13; Mismatches 23; Indels 116; Gaps 2;

Qy 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDTHAIHWKQNP 60
 Db 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTSYNMHWKQTP 60
 Qy 61 GQRLWIGYFSGNDFFKYNRERFKGKATLTADTASTAYVELSLRSRSDTAVYFCTSLN 120
 Db 61 GRGLEWIGAIYFGNDTSYQKFKGKATLTADKSSSTAYMQLSLTSDSAVYICARSTY 120

Qy 121 MA-----YNGQGLTVTVSASTKGPSVFFPLAPSSKSTSGTAAALGCLVKDYFPEPTVS 174
 Db 121 YGSDWYFNWAGTITVTVSAASTKGPSVFFPLAPSSKSTSGTAAALGCLVKDYFPEPTVS 180

Qy 175 WNSGALTSGVHTTPAVLQSSGLYSLSVTVTPSSSLGTQYICNVNHPKSNKTKVDKKEP 234
 Db 181 WNSGALTSGVHTTPAVLQSSGLYSLSVTVTPSSSLGTQYICNVNHPKSNKTKVDKKEP 240

Qy 235 KSCDKTHTCPPCP----- 247
 Db 241 KSCDKTHTCPPCPAPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNW 300

Qy 248 ----- 247
 Db 301 YVDCGEVHNAKTPRERQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIIS 360

Qy 248 ---GQPEPQVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTPPV 304
 Db 361 KAKGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTPPV 420

Qy 305 LDSGSPFLYKSLTVDKSRWQGNVFCSCVMHEALHNNHYTKQSLSPGK 354
 Db 421 LDSGSPFLYKSLTVDKSRWQGNVFCSCVMHEALHNNHYTKQSLSPGK 470

RESULT 6
 ID ABB82832 standard; protein; 470 AA.
 AC ABB82832;
 XX
 DT 31-MAR-2003 (first entry)
 DE Antibody C2B8 heavy chain.
 XX
 KW C2B8; antibody; cytostatic; antiallergic; antianemic; antiasthmatic;
 KW vsotropic; immunomodulator; protozoacide; antidiabetic; nephrotropic;
 KW thyromimetic; hepatotropic; haemostatic; antileptotic; antibacterial;
 KW neuroprotective; antipsoriatic; antirheumatic; antiarthritic; antiulcer;
 KW dermatological; immunosuppressive; antiinflammatory.
 XX
 OS Homo sapiens.
 XX
 XX WO200296948-A2.
 XX
 XX 05-DEC-2002.
 XX
 XX 29-JAN-2002; 2002WO-US002374.
 XX
 XX 29-JAN-2001; 2001US-0264318P.
 XX 16-NOV-2001; 2001US-0331481P.
 XX 21-DEC-2001; 2001US-0341858P.
 XX
 XX (IDEC-) IDEC PHARM CORP.
 XX
 XX Braslawsky GR, Hanna N, Chinn P, Hariharan K;
 XX WPI; 2003-140446/13.
 XX N-PSDB; ABZ24016.
 XX
 XX Novel dimeric antibody useful for treating immune disorder and neoplastic
 XX disorder, has several non-covalently associated monomeric subunits.
 XX
 XX Example 1; Fig 1A; 78pp; English.
 XX
 CC The invention relates to a dimeric antibody (I) comprising several
 CC monomeric subunits, where the monomeric subunits are non-covalently
 CC associated. (I) is useful for treating a disorder, especially immune
 CC disorder, and neoplastic disorder such as relapsed Hodgkin's disease,
 CC resistant Hodgkin's disease high grade, low grade and intermediate grade
 CC non-Hodgkin's lymphomas, B cell chronic lymphocytic leukemia (B-CLL),
 CC lymphoplasmacytoid lymphoma (LPL), mantle cell lymphoma (MCL), follicular
 CC lymphoma (FL), diffuse large cell lymphoma (DLCL), Burkitt's lymphoma,

CC AIDS-related lymphomas, monocytic B cell lymphoma, angioimmunoblastic
CC lymphadenopathy, small lymphocytic, follicular, diffuse large cell,
CC diffuse small cleaved cell, large cell immunoblastic lymphoblastoma,
CC small, non-cleaved, Burkitt's and non-Burkitt's, follicular, mixed small
CC cleaved and large cell lymphomas, in a mammal, (i) is also useful for
CC treating allergic rhinitis, autoimmune haemolytic anemia, allergic
CC contact dermatitis, Addison's disease, atopic dermatitis, amyloidosis,
CC aplastic anemia, arteritis, asthma, ataxia-telangiectasia, autoimmune
CC oophoritis, Buerger's disease, bronchitis, candidiasis, post-myocardial
CC infarction syndrome, carditis, celiac sprue, Chagas's disease, Chediak-
CC Higashi syndrome, Crohn's disease, cryoglobulinemia, diabetes mellitus,
CC erythema multiforme, glomerulonephritis, Goodpasture's syndrome, Grave's
CC disease, Hashimoto's thyroiditis, haemolytic disease of the newborn,
CC hepatitis, idiopathic thrombocytopenic purpura, leprosy, Lyme disease,
CC multiple sclerosis, myasthenia gravis, polymyositis, scleroderma,
CC paroxysmal nocturnal haemoglobinuria, psoriasis, Raynaud's phenomenon/
CC syndrome, rheumatoid arthritis, Sjogren's syndrome, systemic lupus
CC erythematosus, transplant rejection, and ulcerative colitis. (i) is also
CC useful for inducing hyper-cross-linking of membrane antigens, for killing
CC or inhibiting selected cell populations in the treatment of diseases such
CC as cancer and immune disorders, for treating myelosuppressed or
CC myelocompromised patients, for inducing apoptosis in the target cell
CC population or effectively block cell surface receptors necessary for the
CC growth of neoplastic cells, in viral or bacterial neutralization, for
CC diagnostic imaging of tumours, and for reducing tumour size, inhibiting
CC tumour growth and/or prolonging the survival time of tumour-bearing
CC animals. The present sequence represents the antibody C2B8 heavy chain
XX
SQ Sequence 470 AA;

Query Match 86.0%; Score 1614; DB 6; Length 470;
Best Local Similarity 67.7%; Pred. No. 2e-97;
Matches 318; Conservative 13; Mismatches 23; Indels 116; Gaps 2;
QY 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDHAHVKQNP 60
Db 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTSYNMHWKQTP 60
QY 61 GQRLWIGYFPGNDDFKYNRPFKQKATLTADTSASTAYVELSLRSEDYAVYFCTRSIN 120
Db 61 GRGLEWVGAILYFPGNGDTSYNQKPKATLTADKSSSTAYMQLSLTSDSAVYCARSTY 120
QY 121 MA-----YWGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTS 174
Db 121 YGGDWYFNVWGAGTTVTVAATSKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTS 180
QY 175 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVKPEP 234
Db 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKKAEP 240
QY 235 KSDKTHTCPPCP----- 247
Db 241 KSDKTHTCPPCPAPPELLGPGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
QY 248 ----- 247
Db 301 YVDGVEVNAKTPREBQYNSTYRVVSVLTVLHQDLNKGKEYCKVSKNALPAPEKTISK 360
QY 248 ---GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 304
Db 361 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 420
QY 305 LDSGSPFLYSKLTVDKSRWQQGNVFNCSVMHEALHNYHTQKSLSPGK 354
Db 421 LDSGSPFLYSKLTVDKSRWQQGNVFNCSVMHEALHNYHTQKSLSPGK 470

RESULT 7
AAW52156
ID AAW52156 standard; protein; 731 AA.
XX
AC AAW52156;
XX

DT 05-FEB-2002 (first entry)
XX Humanised HMFG-1 heavy chain/DNase I fusion protein 1.
DE
XX Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
XX Homo sapiens.
OS Synthetic.
XX WO200174905-A1.
PN 11-OCT-2001.
PD
XX 26-MAR-2001; 2001WO-GB001324.
XX 03-APR-2000; 2000GB-00008049.
PR 02-OCT-2000; 2000US-0237159P.
XX (ANTI-) ANTISOMA RES LTD.
XX Young RJ;
PI WPI; 2001-662969/76.
XX Novel compound used to treat cancer has target cell-specific portion
PT comprising humanized monoclonal antibody having specificity for
PT polymorphic epithelial mucin, and cytotoxic portion having
PT endonucleolytic activity.
XX Claim 20; Fig 7; 176pp; English.
XX The invention relates to a compound which comprises a target cell-
CC specific portion, comprising an humanised monoclonal antibody, having
CC specificity for polymorphic epithelial mucin (PEM) or its antigen binding
CC fragment and a cytotoxic portion having endonucleolytic activity.
CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The
CC compound has cytostatic activity useful for treating cancer and acting as
CC a potential inducer of apoptosis
XX Sequence 731 AA;

Query Match 86.0%; Score 1613.5; DB 4; Length 731;
Best Local Similarity 67.7%; Pred. No. 3.5e-97;
Matches 316; Conservative 18; Mismatches 20; Indels 113; Gaps 2;
QY 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDHAHVKQNP 60
Db 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFSAYWVQAP 60
QY 61 GQRLWIGYFPGNDDFKYNRPFKQKATLTADTSASTAYVELSLRSEDYAVYFCTRSIN 120
Db 61 GKGLEWVGAILPGSNNSRYNEKFKGRVTVTRDTSTNTAYMELSLRSEDYAVYCARSYD 120
QY 121 ---MAYWQGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNS 177
Db 121 FAWFAYWQGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNS 180
QY 178 GALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVKPEKSC 237
Db 181 GALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVKPEKSC 240
QY 238 DKTHTCPPCP----- 247
Db 241 DKTHTCPPCPAPPELLGPGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 300
QY 248 ----- 247
Db 301 GVEVHNAKTPREBQYNSTYRVVSVLTVLHQDLNKGKEYCKVSKNALPAPEKTISKAK 360
QY 248 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 307
Db 361 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 420

QY 308 DGSFLLYSKLTVDKSRWQGNVFCVSVNHEALHNHYTKSLSPGK 354
 DB 421 DGSFLLYSKLTVDKSRWQGNVFCVSVNHEALHNHYTKSLSPGK 467

RESULT 8
 AAM52159
 ID AAM52159 standard; protein; 741 AA.
 XX
 AC AAM52159;
 XX
 DT 05-FEB-2002 (first entry)
 DE Humanised HMEG-1 heavy chain/DNase I fusion protein 4.
 KW Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
 KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
 OS Homo sapiens.
 OS Synthetic.
 PN WO200174905-A1.
 XX
 PD 11-OCT-2001.
 XX
 PF 26-MAR-2001; 2001WO-GB001324.
 XX
 PR 03-APR-2000; 2000GB-00008049.
 PR 02-OCT-2000; 2000US-0237159P.
 XX
 XX (ANTI-) ANTISOMA RES LTD.
 PA
 PI Young RJ;
 XX
 DR WPI; 2001-662969/76.
 XX
 PT Novel compound used to treat cancer has target cell-specific portion
 PT comprising humanised monoclonal antibody having specificity for
 PT polymorphic epithelial mucin, and cytotoxic portion having
 PT endonucleolytic activity.
 XX
 PS Claim 20; Fig 10; 176pp; English.
 XX
 CC The invention relates to a compound which comprises a target cell-
 CC specific portion, comprising a humanised monoclonal antibody, having
 CC specificity for polymorphic epithelial mucin (PEM) or its antigen binding
 CC fragment and a cytotoxic portion having endonucleolytic activity,
 CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The
 CC compound has cytostatic activity useful for treating cancer and acting as
 CC a potential inducer of apoptosis
 XX
 SQ Sequence 741 AA;

Query Match 86.0%; Score 1613.5; DB 4; Length 741;
 Best Local Similarity 67.7%; Pred. No. 3.6e-97;
 Matches 316; Conservative 18; Mismatches 20; Indels 113; Gaps 2;

QY 1 MGWSLILLFLVAVATRLVSQVQLVQSGAEVVKPGASVKISKASGYTFDTHAIHWKQNP 60
 DB 1 MGWSLILLFLVATATGHSQVQLVQSGAEVVKPGASVKISKASGYTFSAWIEWVRQAP 60

QY 61 GQRLWIGYFGPGNDDFKYNRFKGLATLTADTSASTAYVELSSLRSEDTAVYFCTRLN 120
 DB 61 GKGLEWVGEILLPGSNNSRYNEKGRVTVTRDTSTNTAYMELSSLRSEDTAVYICARSYD 120

QY 121 ---MAYWQGHVTVSSASTGKPSVFPPLAPSKTSSTGTAALGCLVQDYFPEPTVSVNS 177
 DB 121 FAWFAYWQGHVTVSSASTGKPSVFPPLAPSKTSSTGTAALGCLVQDYFPEPTVSVNS 180

QY 178 GALTSGVHTFPAVLQSSGLYSLSSVTVFPSSSLGTQTYICNVNKPSTKVDKVEPKSC 237
 DB 181 GALTSGVHTFPAVLQSSGLYSLSSVTVFPSSSLGTQTYICNVNKPSTKVDKVEPKSC 240

QY 238 DKHTTCCPCP----- 247
 DB 241 DKHTTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 300
 QY 248 ----- 247

DB 301 GVEVHNAKTRPREQYNSYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAK 360
 QY 248 GQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTTPPVLD 307
 DB 361 GQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTTPPVLD 420

QY 308 DGSFLLYSKLTVDKSRWQGNVFCVSVNHEALHNHYTKSLSPGK 354
 DB 421 DGSFLLYSKLTVDKSRWQGNVFCVSVNHEALHNHYTKSLSPGK 467

RESULT 9
 AAB08026
 ID AAB08026 standard; protein; 470 AA.
 XX
 AC AAB08026;
 XX
 DT 12-SEP-2003 (revised)
 DT 14-NOV-2000 (first entry)
 XX
 DE A dimeric anti-CD20 heavy chain polypeptide.
 XX
 KW Anti-CD20 antibody; dimeric immunoglobulin; immunoglobulin; IGG;
 KW complement system; Fc gamma receptor; cytotoxic effector cell;
 KW host immune cell; programmed cell death; allergic disorder; cancer;
 KW autoimmune disease; allergic asthma; atopic dermatitis; Crohn's disease;
 KW allergic bronchopulmonary aspergillosis; allergic rhinitis;
 KW Graves's disease; food allergy; allergic contact dermatitis; cancer;
 KW B-cell lymphoma; rheumatoid arthritis; ulcerative colitis; psoriasis;
 KW pigeon breeder's disease; hepatitis; leprosy; Lyme disease;
 KW diabetes mellitus; candidiasis; aplastic anaemia.
 OS Mus sp.
 OS Homo sapiens.
 OS Chimeric.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /note= "signal peptide"
 FT Protein 20..140
 FT /note= "murine anti-human CD20 heavy chain variable
 FT region"
 FT Protein 141..470
 FT /note= "human gamma 1 heavy chain constant region"
 XX
 PN WO200044788-A1.
 XX
 PD 03-AUG-2000.
 XX
 PF 28-JAN-2000; 2000WO-US001893.
 XX
 PR 28-JAN-1999; 99US-00238741.
 XX
 FA (IDEC-) IDEC PHARM CORP.
 XX
 PI Braslawsky GR, Hanna N, Hariharan K, Labarre MJ, Huynh TB;
 XX WPI; 2000-514811/46.
 DR N-PSDB; AAA63531.
 DR
 XX Genetically engineering immunoglobulin (Ig) G/IgG dimers for the
 PT treatment of cancers, allergic disorders and autoimmune conditions.
 XX
 PS Example 1; Fig 2A-C; 65pp; English.
 XX
 CC The present sequence represents a dimeric anti-CD20 light chain

polypeptide. The dimeric immunoglobulin is used in the method of the invention. The specification describes a method for producing an immunoglobulin (Ig) G/IgG dimer. The method comprises genetically engineering a monoclonal antibody to introduce a cysteine molecule which inhibits formation of intramolecular disulphide bridges between sister heavy chains on the same antibody molecule. The dimer is a homodimer or heterodimer that is capable of activating components of the complement system, and has the ability to activate and kill cells via the complement cascade. The dimer is also capable of binding to Fc gamma receptors on cytotoxic effector cells and on host immune cells, and is capable of initiating programmed cell death. The IgG/IgG dimers may be used to treat allergic disorders, cancers and autoimmune diseases such as allergic asthma, allergic bronchopulmonary aspergillosis, allergic rhinitis, atopic dermatitis, Crohn's disease, Graves's disease, food allergies, allergic contact dermatitis, CLL cancers and/or B-cell lymphomas. They may also be used to treat a range of other diseases and disorders such as rheumatoid arthritis, ulcerative colitis, psoriasis, pigeon breeder's disease, hepatitis, leprosy, Lyme disease, diabetes mellitus, candidiasis and aplastic anaemia. They are also useful for inducing hyper-cross-linking of membrane antigens and for the preferential killing of selected cell populations. (Updated on 12-SEP-2003 to standardise OS field)

XX SQ Sequence 470 AA;

Query Match 86.0%; Score 1613; DB 3; Length 470;
 Best Local Similarity 67.7%; Pred. No. 2.3e-97;
 Matches 318; Conservative 13; Mismatches 23; Indels 116; Gaps 2;

Qy 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDHAHVKVQNP 60
 Db 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTSYNHWVKQTP 60
 Qy 61 GQRLWIGYFSPGNDFFKYNRFGKATLTADTSASTAYVELSLRSSEDTAVYFCTRSLN 120
 Db 61 GRGLEWIGALYPGNGDTSYNOKFKGATLTADTSASTAYMQLSSLTSDSAVYICARSTY 120
 Qy 121 MA-----YMGQGLTVTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVVS 174
 Db 121 YGGDWYFNVWGAGTTVTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVVS 180
 Qy 175 WNSGALTSQVHTFPFPAVLQSSGLYSLSVTVVPSSSLGTQTYICNVNHKPSNTKVDKKVEP 234
 Db 181 WNSGALTSQVHTFPFPAVLQSSGLYSLSVTVVPSSSLGTQTYICNVNHKPSNTKVDKKVEP 240
 Qy 235 KCDKTHTCPPCP----- 247
 Db 241 KCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW 300
 Qy 248 ----- 247
 Db 301 YVDGVEVHNAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
 Qy 248 --GQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEVESGQPNNYKTTTPPV 304
 Db 361 KAKGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEVESGQPNNYKTTTPPV 420
 Qy 305 LDSGSPFLYSLKLTVDKSRWQGGNVFSCVMHEALHNHYTQKSLSLSPGK 354
 Db 421 LDSGSPFLYSLKLTVDKSRWQGGNVFSCVMHEALHNHYTQKSLSLCPGK 470

RESULT 10
 AAM52158
 ID AAM52158 standard; protein; 729 AA.
 AC AAM52158;
 XX
 XX 05-FEB-2002 (first entry)
 DT Humanised HMFG-1 heavy chain/DNase I fusion protein 3.
 DE Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
 XX cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
 KW

XX Homo sapiens.
 OS Synthetic.
 OS WO200174905-A1.
 PN 11-OCT-2001.
 PD 26-MAR-2001; 2001WO-GB001324.
 PF 03-APR-2000; 2000GB-00008049.
 PR 02-OCT-2000; 2000US-0237159P.
 XX (ANTI-) ANTISOMA RES LTD.
 XX Young RJ;
 WIPI; 2001-662969/76.
 Novel compound used to treat cancer has target cell-specific portion comprising humanized monoclonal antibody having specificity for polymorphic epithelial mucin, and cytotoxic portion having endonucleolytic activity.
 Claim 20; Fig 9; 176pp; English.
 The invention relates to a compound which comprises a target cell-specific portion, comprising an humanised monoclonal antibody, having specificity for polymorphic epithelial mucin (PEM) or its antigen binding fragment and a cytotoxic portion having endonucleolytic activity. The compound is exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The compound has cytostatic activity useful for treating cancer and acting as a potential inducer of apoptosis
 Sequence 729 AA;

Query Match 85.7%; Score 1608.5; DB 4; Length 729;
 Best Local Similarity 67.6%; Pred. No. 7.5e-97;
 Matches 315; Conservative 18; Mismatches 20; Indels 113; Gaps 2;

Qy 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDHAHVKVQNP 60
 Db 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFSAYWIEWVRQAP 60
 Qy 61 GQRLWIGYFSPGNDFFKYNRFGKATLTADTSASTAYVELSLRSSEDTAVYFCTRSLN 120
 Db 61 GKGLEWVGEILPGSNNGRYNEKFKGRVTVTRDTSTNTAYMELSLRSSEDTAVYICARSYD 120
 Qy 121 ---MAYWGQGLTVTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVVS 177
 Db 121 FAWFAYWGQGLTVTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVVS 180
 Qy 178 GALTSGVHTFPFPAVLQSSGLYSLSVTVVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC 237
 Db 181 GALTSGVHTFPFPAVLQSSGLYSLSVTVVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC 240
 Qy 238 DKTHTCPPCP----- 247
 Db 241 DKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVD 300
 Qy 248 ----- 247
 Db 301 GVEVHNAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 360
 Qy 248 GQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEVESGQPNNYKTTTPPVLD 307
 Db 361 GQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEVESGQPNNYKTTTPPVLD 420
 Qy 308 DGSFPLYSKLTVDKSRWQGGNVFSCVMHEALHNHYTQKSLSLSPG 353
 Db 421 DGSFPLYSKLTVDKSRWQGGNVFSCVMHEALHNHYTQKSLSLSPG 466

XX New antibodies and proteins bind conserved epitope of Fas antigen - used
PT to evaluate drugs in animal models and to treat Fas-associated diseases
PT e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis,
XX hepatitis and AIDS.
XX
PS Claim 22; Page 212-213; 292pp; English.
XX
CC This is the amino acid sequence of the VD type humanised heavy chain of
CC murine anti-human Fas monoclonal antibody HFE7A. E. coli pGSHSLA62 SANK
CC 73397 harbors plasmid pGSHSLA62 carrying a fusion fragment of the
CC humanised VD type HFE7A heavy chain and DNA encoding human IgG1 constant
CC region (see AAV70079), and is deposited as FERM BP-6074 (claimed). The
CC invention provides methods for producing humanised antibodies by
CC culturing host cells. Humanised versions of HFE7A (see AAW83031-37), like
CC native HFE7A, are capable of inducing apoptosis in abnormal cells
CC expressing Fas, and of inhibiting Fas-induced apoptosis in normal cells.
CC The humanised antibodies are used to evaluate, in animal models,
CC treatments of diseases that involve Fas/Fas ligand interactions, and also
CC to treat such diseases, including autoimmune disease (e.g. systemic lupus
CC erythematosus, Hashimoto's disease, graft versus host disease, Sjogren
CC syndrome, pernicious anaemia, Addison's disease, scleroderma, Goodpasture
CC syndrome, Crohn's disease, rheumatoid arthritis, autoimmune haemolytic
CC anaemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's
CC disease, thrombopenia purpura and insulin-dependent diabetes), allergies,
CC atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular
CC nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection
CC (all claimed). (Updated on 25-MAR-2003 to correct DR field.)
XX
SQ Sequence 470 AA;

Query Match 85.4%; Score 1603; DB 2; Length 470;
Best Local Similarity 67.0%; Pred. No. 1e-96;
Matches 315; Conservative 17; Mismatches 22; Indels 116; Gaps 2;
QY 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASYTFTDTHAIHWKQNP 60
DB 1 MGWSLILFLVATATGTVHVSQVQLVQSGAEVVKPGASVKISKASYTFTSYMQWVKQAP 60
QY 61 QORLEWIGYFSGNDDFKYNRPFKQKATLTADTASTAYVELSLRSEDYAVYFCTRSIN 120
DB 61 QORLEWIGMGEIDPDSYTYNQNKFQKATLTVDTSASTAYMELSLRSEDYAVYCARND 120
QY 121 MA-----YMGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVVS 174
DB 121 YSNWNYFDVWEGEGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVVS 180
QY 175 WNSGALTSQVHTFPFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKSNTKVDKVEP 234
DB 181 WNSGALTSQVHTFPFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKSNTKVDKVEP 240
QY 235 KSCDKTHTCPPCP----- 247
DB 241 KSCDKTHTCPPCPAPPELLGGPSVFLFPPKPTLMISRTPEVTCVVDVSHEDPEVKFNW 300
QY 248 ----- 247
DB 301 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDLNGLKEPKCKVSKNALPAPIETKIS 360
QY 248 ---GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 304
DB 361 KAKGQPREPQVYTLPPSRDEMTKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 420
QY 305 LDSGGSFFLYSKLTVDKSRWQGNVFNCSVMHEALHNYHTQKLSLSFGK 354
DB 421 LDSGGSFFLYSKLTVDKSRWQGNVFNCSVMHEALHNYHTQKLSLSFGK 470
RESULT 13
AAB14776
ID AAB14776 standard; protein; 470 AA.
XX
AC AAB14776;

XX 12-SEP-2003 (revised)
DT 24-NOV-2000 (first entry)
XX
DE Humanised anti-Fas antibody heavy chain, SEQ ID NO:89.
XX
KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828; murine;
KW humanised antibody; complementarity determining region; CDR; human Fas;
KW Fas ligand; apoptosis modulator; programmed cell death;
KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancyelophthisis;
KW hepatitis; AIDS; graft rejection; heavy chain.
XX
OS Mus musculus.
OS Homo sapiens.
OS Chimeric.
XX
PN JP2000169393-A.
XX
PD 20-JUN-2000.
XX
PF 30-SEP-1999; 99JP-00278301.
XX
PR 30-SEP-1998; 98JP-00276883.
XX
PA (SANY) SANKYO CO LTD.
XX
XX WPI; 2000-485645/43.
DR N-PSDB; AAA72159.
XX
PT Preventive or treating agent for the diseases caused by an abnormality in
PT the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas
PT antibody.
PS Claim 21; Page 95-96; 139pp; Japanese.
XX
CC The invention relates to compositions for the prevention or treatment or
CC diseases caused by an abnormality in the Fas/Fas ligand system containing
CC an anti-Fas antibody as the active component. The anti-Fas antibody is
CC either the murine anti-human Fas monoclonal antibody HFE7A, or a
CC humanised version of HFE7A containing identical CDRs (complementarity
CC determining regions) to antibody HFE7A. Via its interaction with Fas, the
CC antibody of the invention acts as a modulator of apoptosis. The
CC compositions of the invention may therefore be used in the treatment or
CC prevention of conditions such as autoimmune diseases, allergy, atopy,
CC arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis,
CC aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft
CC rejection. Sequences AAB14775-B14776 and AAB14779 represent the heavy
CC chains (or fragments thereof) of various humanised HFE7A-derived anti-Fas
CC antibodies. (Updated on 12-SEP-2003 to standardise OS field)
XX
SQ Sequence 470 AA;
Query Match 85.4%; Score 1603; DB 3; Length 470;
Best Local Similarity 67.0%; Pred. No. 1e-96;
Matches 315; Conservative 17; Mismatches 22; Indels 116; Gaps 2;
QY 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASYTFTDTHAIHWKQNP 60
DB 1 MGWSLILFLVATATGTVHVSQVQLVQSGAEVVKPGASVKISKASYTFTSYMQWVKQAP 60
QY 61 QORLEWIGYFSGNDDFKYNRPFKQKATLTADTASTAYVELSLRSEDYAVYFCTRSIN 120
DB 61 QORLEWIGMGEIDPDSYTYNQNKFQKATLTVDTSASTAYMELSLRSEDYAVYCARND 120
QY 121 MA-----YMGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVVS 174
DB 121 YSNWNYFDVWEGEGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVVS 180
QY 175 WNSGALTSQVHTFPFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKSNTKVDKVEP 234
DB 181 WNSGALTSQVHTFPFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKSNTKVDKVEP 240

QY 235 KSCDKTHCTCPCP----- 247
 DB 241 KSCDKTHCTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW 300
 QY 248 ----- 247
 DB 301 YVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
 QY 248 ---GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEVESNGQPENNYKTTPPV 304
 DB 361 KAKGQPREPQVYTLPPSRDEMTKQVSLTCLVKGFYPSDIAVEVESNGQPENNYKTTPPV 420
 QY 305 LDSGSPFLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 354
 DB 421 LDSGSPFLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470

RESULT 14

AAW90926
 ID AAW90926 standard; protein; 470 AA.

AC AAW90926;

DT 08-AUG-2000 (first entry)

Humanised HFE7A designed heavy chain protein.

Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
 dermatological; immunosuppressive; thymine; antirheumatic; anti-Fas;
 nephrotropic; humanized; neuroprotective; antirheumatic; anti-Fas;
 Hashimoto disease; rheumatoid arthritis; systemic lupus erythematosus;
 Sjogren's syndrome; anemia; Addison's disease; graft versus host disease;
 Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 Synthetic.

OS EP990663-A2.

PN 05-APR-2000.

PD 29-SEP-1999; 99EP-00307711.

PF 30-SEP-1998; 98JP-00276881.

PR 30-SEP-1998; 98JP-00276882.

XX (SANY) SANKYO CO LTD.

PI Serizawa N, Haryuana H, Nakahara K, Tamaki I, Takahashi T;

XX WPI; 2000-258930/23.

DR N-ESDB; AAA11597.

PT New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems.

XX Example reference 15; Page 134-136; 263pp; English.

XX This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thymine, antirheumatic,
 CC antinephrotropic, nephrotropic, antiinfertility, neuroprotective,
 CC antiarteriosclerotic, cardiant and hepatotropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive

CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjogren's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody HFE7A designed heavy chain which is used in
 CC the method described in the invention

XX SQ Sequence 470 AA;

Query Match 85.4%; Score 1603; DB 3; Length 470;
 Best Local Similarity 67.0%; Pred. No. 1e-96;
 Matches 315; Conservative 17; Mismatches 22; Indels 116; Gaps 2;

QY 1 MGWSLILFLVAVATRVLSQVLVQSGAEVVKPGASVKISKASGYTFTDHAHHWKNP 60
 DB 1 MGWSLILFLVATATGVHSQVLVQSGAEVVKPGASVKISKASGYTFTSYWQWVKQAP 60

QY 61 GQRLWGYSPGNDDEFKYNRFGKATLTADTSASTAYVELSLRSEDTAVFCTSLN 120

DB 61 GQRLWGYSPGNDDEFKYNRFGKATLTADTSASTAYVELSLRSEDTAVFCTSLN 120

QY 121 MA-----YMGQGLTVTVSSASTKPSVFPPLAPSSKTSSTGTAALGCLVKDYFPEPTVS 174

DB 121 YSNWYFDVWGEGLTVTVSSASTKPSVFPPLAPSSKTSSTGTAALGCLVKDYFPEPTVS 180

QY 175 WNSGALSGVHTFPAPVLOSGSLVSLSVTVVPSSSLGTQTYICNNHKKPSNTKVDKKVEP 234

DB 181 WNSGALSGVHTFPAPVLOSGSLVSLSVTVVPSSSLGTQTYICNNHKKPSNTKVDKKVEP 240

QY 235 KSCDKTHCTCPCP----- 247

DB 241 KSCDKTHCTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW 300

QY 248 ----- 247

DB 301 YVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360

QY 248 ---GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEVESNGQPENNYKTTPPV 304

DB 361 KAKGQPREPQVYTLPPSRDEMTKQVSLTCLVKGFYPSDIAVEVESNGQPENNYKTTPPV 420

QY 305 LDSGSPFLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 354

DB 421 LDSGSPFLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470

RESULT 15

ABB74941

ID ABB74941 standard; protein; 470 AA.

XX ABB74941;

XX 30-APR-2002 (first entry)

DT Humanised anti-Fas antibody light chain SEQ ID NO 50.

DE Human; mouse; Fas/Fas ligand system; Fas; antibody; light chain;

KW heavy chain; apoptosis; anti-allergic; immunosuppressive; apoptotic;

KW autoimmune disease; allergy; atopy.

XX Synthetic.

XX

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FN JP2001342149-A.
XX
XX
PD 11-DEC-2001.
XX
XX
PF 28-MAR-2001; 2001JP-00093243.
XX
XX
PR 29-MAR-2000; 2000JP-00091144.
XX
XX
PA (SANY ) SANKYO CO LTD.
XX
XX
DR WPI; 2002-145114/19.
DR N-PSDB; ABL48674.
XX
XX
PT Drug for preventing or treating e.g. autoimmune disease or allergy,
PT comprises humanized anti-Fas antibody.
XX
XX
PS Example 14 (preparatory); Page 79; 154pp; Japanese.
XX
XX
CC The invention relates to a preventive or treating agent for diseases
CC caused by abnormality in the Fas/Fas ligand system containing, as the
CC active component, an antibody having a light chain subunit and a heavy
CC chain subunit and an activity of combining specifically with mammalian
CC Fas and an activity of inducing apoptosis in a cell expressing Fas. The
CC agent has anti-allergic, immunosuppressive and apoptotic activity and is
CC used for preventing and treating autoimmune diseases, allergy, atopy and
CC others
XX
XX
SQ Sequence 470 AA;
Query Match 85.4%; Score 1603; DB 5; Length 470;
Best Local Similarity 67.0%; Pred. No. 1e-96;
Matches 315; Conservative 17; Mismatches 22; Indels 116; Gaps 2;

Qy 1 MGWSLILFLVAVATRVLSQVLVQSGAEVVKPGASVKISKASGYTFDTHAIHWKQNP 60
Db 1 MGWSLILFLVAVATRVLSQVLVQSGAEVVKPGASVKISKASGYTFDTHAIHWKQNP 60
Qy 61 GORLEWICYFSPGNDPFKYNREKFKATLTADTSASTAYVELSLRSEDATAYECTRLN 120
Db 61 GORLEWGEIDPSYTYNOKFKGATLTVDTSASTAYMELSLRSEDATAYCYARNRD 120
Qy 121 MA-----YMGQGLTVTVSSASTKGPSVFPLAPSKSTSGTAAALGCLVKDYFPEPTVS 174
Db 121 YSNWYFDVWGEGLTVTVSSASTKGPSVFPLAPSKSTSGTAAALGCLVKDYFPEPTVS 180
Qy 175 WNSGALTSQVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNKKPSNTKYDKVEP 234
Db 181 WNSGALTSQVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNKKPSNTKYDKVEP 240
Qy 235 KSCDKTHTCPCP----- 247
Db 241 KSCDKTHTCPCPAPPELLGSPVFLFPPKPKDTLMI SRTPEVTCVVDVSHEDPEVKFNW 300
Qy 248 ----- 247
Db 301 YVDGVEVHNATKPREQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIIS 360
Qy 248 ---GQPREPQVYTLPPSDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 304
Db 361 KAKGQPREPQVYTLPPSDEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 420
Qy 305 LDSGSPFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 354
Db 421 LDSGSPFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 470

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Search completed: March 23, 2005, 18:34:43
Job time : 144.455 secs

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OM protein - protein search, using sw model

Run on: March 23, 2005, 18:11:05 ; Search time 36.3535 Seconds
(without alignment)
726.911 Million cell updates/sec

Title: US-10-058-069-7

Perfect score: 1876

Sequence: 1 MGWSLILFLVAVATRVLSQ.....MHEALHNHYTKSLSLSPGK 354

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pap.*
- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pap.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pap.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pap.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pap.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1559	83.1	466	4	US-09-698-705-11
2	1549	82.6	472	4	US-09-301-593-43
3	1541	82.1	449	1	US-08-458-516-13
4	1524	81.2	472	4	US-09-301-593-30
5	1506	80.3	476	2	US-08-378-939-10
6	1501	80.0	468	3	US-09-485-737B-67
7	1501	80.0	468	4	US-10-071-485-67
8	1501	80.0	711	3	US-09-485-737B-90
9	1501	80.0	711	4	US-10-071-485-90
10	1495.5	79.7	467	3	US-09-049-672A-8
11	1486.5	79.2	453	4	US-09-301-593-18
12	1485	79.2	462	4	US-09-627-896B-24
13	1485	79.2	478	3	US-08-487-550-8
14	1485	79.2	478	4	US-09-526-098-8
15	1485	79.2	478	4	US-09-383-916-8
16	1481.5	79.0	452	3	US-09-027-449-71
17	1481.5	79.0	452	3	US-09-026-985-71
18	1481.5	79.0	452	4	US-09-121-952A-71
19	1481.5	79.0	452	4	US-09-234-340A-71
20	1480.5	78.9	454	2	US-07-934-373C-22
21	1480.5	78.9	454	3	US-08-437-642B-22
22	1480.5	78.9	454	4	US-08-146-206C-22
23	1480.5	78.9	454	4	US-09-705-686-22
24	1480.5	78.9	454	4	US-09-705-392A-22
25	1480.5	78.9	454	4	US-09-705-398-22
26	1480.5	78.9	454	5	PCT-US93-07832-22
27	1462	77.9	451	3	US-09-247-352-3

28 1462 77.9 451 4 US-09-466-635-3 Sequence 3, Appli
29 1459.5 77.8 467 4 US-08-030-175-41 Sequence 41, Appli
30 1455.5 77.6 467 4 US-08-030-175-42 Sequence 42, Appli
31 1444 77.0 470 4 US-09-859-053-28 Sequence 28, Appli
32 1440.5 76.8 449 3 US-09-679-397-2 Sequence 2, Appli
33 1440.5 76.8 449 4 US-09-680-148-2 Sequence 2, Appli
34 1440.5 76.8 449 4 US-09-304-465A-2 Sequence 2, Appli
35 1436.5 76.6 467 2 US-07-916-098A-45 Sequence 45, Appli
36 1431.5 76.3 475 4 US-09-740-002-25 Sequence 25, Appli
37 1425.5 76.0 475 4 US-09-740-002-27 Sequence 27, Appli
38 1418.5 75.6 459 1 US-08-157-101A-7 Sequence 7, Appli
39 1418.5 74.9 469 2 US-07-934-373C-23 Sequence 23, Appli
40 1404.5 74.9 469 3 US-08-437-642B-23 Sequence 23, Appli
41 1404.5 74.9 469 4 US-08-146-206C-23 Sequence 23, Appli
42 1404.5 74.9 469 4 US-09-705-686-23 Sequence 23, Appli
43 1404.5 74.9 469 4 US-09-705-392A-23 Sequence 23, Appli
44 1404.5 74.9 469 4 US-09-705-398-23 Sequence 23, Appli
45 1402.5 74.8 446 3 US-08-397-411-7 Sequence 7, Appli

ALIGNMENTS

RESULT 1

US-09-698-705-11

; Sequence 11, Application US/09698705

; Patent No. 6824780

; GENERAL INFORMATION:

; APPLICANT: Devaux, B.

; APPLICANT: Keller, G.

; APPLICANT: Koepfen, H.

; APPLICANT: Laaky, L.

; TITLE OF INVENTION: Anti-Tumor Antibody Compositions and Methods of Use

; FILE REFERENCE: P17771

; CURRENT APPLICATION NUMBER: US/09/698,705

; PRIOR FILING DATE: 2000-10-27

; PRIOR APPLICATION NUMBER: US 60/162,558

; PRIOR FILING DATE: 1999-10-29

; PRIOR APPLICATION NUMBER: US 60/182,872

; PRIOR FILING DATE: 2000-02-16

; NUMBER OF SEQ ID NOS: 25

; SEQ ID NO 11

; LENGTH: 466

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: sequence is chimeric mouse/human

US-09-698-705-11

Query Match 83.1%; Score 1559; DB 4; Length 466;

Best Local Similarity 65.5%; Pred. No. 7,7e-112;

Matches 305; Conservative 21; Mismatches 28; Indels 112; Gaps 2;

Qy 1 MGWSLILFLVAVATRVLSQVQVQSGAEVVKPGASVKISKASGYFTDHAHVKNP 60
Db 1 MGWSLILFLVAVATRVLSQVQVQSGAEVVKPGASVKISKASGYFTDHAHVKNP 60
Qy 61 GQRLWIGYFSPGNDFFKYNRFGKATLTADTASATYVELSLRSSEDTAVYFC--TRS 118
Db 61 GQRLWIGYFSPGNDFFKYNRFGKATLTADTASATYVELSLRSSEDTAVYFC--TRS 118
Qy 119 LNMAYWGGLTVTVSSASTKGPSVFPPLAPSSKTSGGTAALGCLVVKDYFPFPVTVMSNG 178
Db 121 YAMAYWGGLTVTVSSASTKGPSVFPPLAPSSKTSGGTAALGCLVVKDYFPFPVTVMSNG 180
Qy 179 ALTSGVHTFFAVLOSSGLYSLSSVTVVPSLSGLGTQYICNVNHPKSNKVDKKVEPKSCD 238
Db 181 ALTSGVHTFFAVLOSSGLYSLSSVTVVPSLSGLGTQYICNVNHPKSNKVDKKVEPKSCD 240
Qy 239 KTHTCPPCP----- 247
Db 241 KTHTCPPCPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDYG 300

QY 248 -----G 248
Db 301 VEVNNAKTPREEQYNTYRVVSVLTVLHQDLNKGKEYCKVSNKALPAPIETKTSKAG 360
QY 249 QPREPOVYTLPSRDELTKNOVSLTCLVKGYPSPDIAVEWESNGQPNENYKTTTPVLDS 308
Db 361 QPREPOVYTLPSREEMTKNOVSLTCLVKGYPSPDIAVEWESNGQPNENYKTTTPVLDS 420
QY 309 GSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTKSLSLSPGK 354
Db 421 GSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTKSLSLSPGK 466
RESULT 2
US-09-301-593-43
; Sequence 43, Application US/09301593A
; Patent No. 6455677
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.1890001
; CURRENT APPLICATION NUMBER: US/09/301,593A
; EARLIER FILING DATE: 1999-04-29
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 43
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-301-593-43
Query Match 82.6%; Score 1549; DB 4; Length 472;
Best Local Similarity 65.3%; Pred. No. 4.6e-111; Indels 120; Gaps 3;
Matches 309; Conservative 15; Mismatches 29;
QY 1 MGWSLILFLVAVATRVLSQVLQSGAEVVKPGASVKISKASGYFTDHAHVKQNP 60
Db 1 MDWTWRVFLLAAPGAHSQVLQSGAEVVKPGASVKISKASGYFTDHAHVKQNP 60
QY 61 GQRLWIGYFSPGNDDFKYNRPKATLTADTSASTAYVELSLRSEDVAVFCTR--- 117
Db 61 GQRLWIGGINPNNGIPNNGKGRATLTGVKASASTAYVELSLRSEDVAVYCARRRI 120
QY 118 -----SLNMAWQGGTLVTVSSASTKGPSVFPLAPSKSTSGGTAALGCLVKDYFPEPV 171
Db 121 AYGDEGHANDYWGQGLTVTVSS--STKGPSVFPLAPSKSTSGGTAALGCLVKDYFPEPV 179
QY 172 TVSNWNGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKK 231
Db 180 TVSNWNGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKK 239
QY 232 VEPKSCDKTHTCPCPCP----- 247
Db 240 VEPKSCDKTHTCPCPCAPPELLAGPSVFLFPPKPKDTLMISTRPEVTCVVDVSHEDPEVK 299
QY 248 ----- 247
Db 300 FNWTVGDVEVNAKTPREEQYNTYRVVSVLTVLHQDLNKGKEYCKVSNKALPAPIEK 359
QY 248 -----GQPREPOVYTLPPSRDELTKNOVSLTCLVKGYPSPDIAVEWESNGQPNENYKTT 301
Db 360 TISKAKGQPREPOVYTLPPSRDEMTKNOVSLTCLVKGYPSPDIAVEWESNGQPNENYKTT 419
QY 302 PPVLDSGSPFLYSLKLTVDKSRWQGNVFCSCVMHEALHNNHYTKSLSLSPGK 354

Db 420 PPVLDSGSPFLYSLKLTVDKSRWQGNVFCSCVMHEALHNNHYTKSLSLSPGK 472
RESULT 3
US-08-458-516-13
; Sequence 13, Application US/08458516
; Patent No. 5777085
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GPIIB/IIIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,159
; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 449 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-458-516-13
Query Match 82.1%; Score 1541; DB 1; Length 449;
Best Local Similarity 67.5%; Pred. No. 1.8e-110;
Matches 303; Conservative 10; Mismatches 22; Indels 114; Gaps 2;
QY 20 QVQLVQSGAEVVKPGASVKISKASGYFTDHAHVKQNPQORLEWIGYFSPGNDDFKY 79
Db 1 QVQLVQSGAEVVKPGASVKISKASGYFTNYLIEWRQAPGOGLEWIGYVPGSGGTNY 60
QY 80 NERFKGKATLTADTSASTAYVELSLRSEDVAVFCTRSNLN---MAYWQGGTLTVVSSA 135
Db 61 NERFKGRVTLTVDESINTAYVELSLRSEDVAVFCARRDNGYGFAYWQGGTLTVVSSA 120
QY 136 STKGPSVFPLAPSKSTSGGTAALGCLVKDYFPEPVTVSNWNGALTSGVHTFPAVLQSSG 195
Db 121 STKGPSVFPLAPSKSTSGGTAALGCLVKDYFPEPVTVSNWNGALTSGVHTFPAVLQSSG 180
QY 196 LYSLSVSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPCP----- 247
Db 181 LYSLSVSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPCAPPELLGGP 240
QY 248 ----- 247
Db 241 SVFLFPPKPKDTLMISTRPEVTCVVDVSHEDPEVKFNWTVGDVEVNAKTPREEQYNS 300

Qy 248 -----GOPREPOVYTLPPSRDEL 265
Db 301 TYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRPEQVYTLPPSRDEL 360
Qy 266 TKNQSVLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRWQ 325
Db 361 TKNQSVLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRWQ 420
Qy 326 QGNVFCSCVMHEALHNHYTQKSLSLSPGK 354
Db 421 QGNVFCSCVMHEALHNHYTQKSLSLSPGK 449
RESULT 4
US-09-301-593-30
; Sequence 30, Application US/09301593A
; Patent No. 6455677
; GENERAL INFORMATION:
; APPLICANT: Park, John B.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: PAP-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.1890001
; CURRENT APPLICATION NUMBER: US/09/301.593A
; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086,049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 30
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-301-593-30
Query Match 81.2%; Score 1524; DB 4; Length 472;
Best Local Similarity 63.8%; Pred. No. 3.8e-109;
Matches 302; Conservative 20; Mismatches 31; Indels 120; Gaps 3;
Qy 1 MGWSLILLFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYFTTDAIHVVKQNP 60
Db 1 MGWSVFLFLSGTAGVLSVQLQSGPELVKPGASVKMSCKTSRYTFTETIHWVRQSH 60
Qy 61 GQRLWIGYFSPGNDDFKYNREFKGKATLTADTSATYVELSLRSRSEDATVYFCTR--- 117
Db 61 GKSLEWIGGINPNIPIYNOQKGRATLTVGKSSSTAYMELSRSLTSDSAVYFCARRRI 120
Qy 118 -----SLNMAWYOGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV 171
Db 121 AYGDEGHAMDYWGQGTSTVTS--STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV 179
Qy 172 TVSNWNGSALTSGVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHNKPSNTKVDKK 231
Db 180 TVSNWNGSALTSGVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHNKPSNTKVDKK 239
Qy 232 VEPKSCDKTHTCPCP----- 247
Db 240 VEPKSCDKTHTCPCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVDVSHEDPEVK 299
Qy 248 ----- 247
Db 300 FNNYVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEK 359
Qy 248 -----GOPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 301
Db 360 TISKAKGQPREPQVYTLPPSRDEETKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 419
Qy 302 PPVLDSDGSGFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 354

Db 420 PPVLDSDGSGFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 472
RESULT 5
US-08-378-939-10
; Sequence 10, Application US/08378939
; Patent No. 5876961
; GENERAL INFORMATION:
; APPLICANT: CROWE, JAMES SCOTT
; APPLICANT: LEWIS, ALAN PETER
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS: 46
; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
; STREET: 555 THIRTEENTH ST. N.W.
; CITY: WASHINGTON
; STATE: D. C.
; COUNTRY: U.S.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/378,939
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US 07/952640
; FILING DATE: 01-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, BARBARA G
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1808-118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-378-939-10
Query Match 80.3%; Score 1506; DB 2; Length 476;
Best Local Similarity 63.4%; Pred. No. 9.3e-108;
Matches 302; Conservative 20; Mismatches 32; Indels 122; Gaps 3;
Qy 1 MGWSLILLFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYFTTDAIHVVKQNP 60
Db 1 MDWTRFLVFAAATGVSQVQVQSGAEVVKPGSSVTVSCASGGTFSNVAISWRQAP 60
Qy 61 GQRLWIGYFSPGNDDFKYNREFKGKATLTADTSATYVELSLRSRSEDATVYFCT--- 116
Db 61 GQGLEWNGGIPLFGTPTYSQNFQGRVTITADKSTSTAHMELTSLRSEDATVYCATDRI 120
Qy 117 RSLNMAWYOGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF 168
Db 121 RQAFDRARVGVDFPQWQGTTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF 180
Qy 169 EPVTVSNWNGSALTSGVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHNKPSNTKV 228
Db 181 EPVTVSNWNGSALTSGVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHNKPSNTKV 240
Qy 229 DKKVEPKSCDKTHTCPCP----- 247
Db 241 DKKVEPKSCDKTHTCPCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVDVSHEDP 300
Qy 248 ----- 247

Db 301 EVKFNWYDGVVEVHNAKTPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
QY 248 -----GPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNY 298
Db 361 LEKTSKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNY 420
QY 299 KTTTPVLSDSGSFYLYSKLTVDKSRWQQGNVFPSCSVMEALHNHYTQKSLSLSPGK 354
Db 421 KTTTPVLSDSGSFYLYSKLTVDKSRWQQGNVFPSCSVMEALHNHYTQKSLSLSPGK 476

RESULT 6
US-09-485-737B-67
; Sequence 67, Application US/09485737B
; Patent No. 6350860
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/09/485,737B
; CURRENT FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 67
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-09-485-737B-67

Query Match 80.0%; Score 1501; DB 3; Length 468;
Best Local Similarity 63.8%; Pred. No. 2.2e-107;
Matches 294; Conservative 24; Mismatches 31; Indels 112; Gaps 2;

QY 6 ILLFLVAVATRVLSQVLQVQSGAEVVKPGASVKISKASGYTFTDTHAIHWYKQNPQGRLE 65
Db 7 IFSFLLISASVILLQVQSGSELKPKGASVKISKASGYTFTDYGNNWVKQAPGQGLK 66
QY 66 WIGYFSPGNDDFKNERFKGKATLTADTSASTAYVELSLRSEDTAYFCTRS--LNWAY 123
Db 67 WMGWINTYTGSTYVDDFKGRFVFLSDTSVSAAYLQISSLKAEDEATYFCARRGFYAMDY 126
QY 124 WGQGLTVTVSSASTKGPSVFLAPSSKSTSGTAAALGCLVKDYFPEPVTYVSWNSGALTSG 183
Db 127 WGQGLTVTVSSASTKGPSVFLAPSSKSTSGTAAALGCLVKDYFPEPVTYVSWNSGALTSG 186
QY 184 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKKEPKSCDKTHTC 243
Db 187 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKKEPKSCDKTHTC 246
QY 244 PPCP----- 247
Db 247 PPCPAPELLGGPSVFLFPPPKPDTLMISRTPEVTCVVDVDSHEDPEVKFNWYVDGVEVHN 306
QY 248 -----GPREP 253
Db 307 AKTAPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTIKAKGQPREP 366
QY 254 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLDSDGSFFL 313
Db 367 QVYTLPPSRDEMTKQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLDSDGSFFL 426
QY 314 YSKLTVDKSRWQQGNVFPSCSVMEALHNHYTQKSLSLSPGK 354
Db 421 YSKLTVDKSRWQQGNVFPSCSVMEALHNHYTQKSLSLSPGK 476

Db 427 YSKLTVDKSRWQQGNVFPSCSVMEALHNHYTQKSLSLSPGK 467

RESULT 7
US-10-071-485-67
; Sequence 67, Application US/10071485
; Patent No. 6830752
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC
; TITLE OF INVENTION: SHOCK,
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/10/071,485
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 09/485,737
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 67
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-10-071-485-67

Query Match 80.0%; Score 1501; DB 4; Length 468;
Best Local Similarity 63.8%; Pred. No. 2.2e-107;
Matches 294; Conservative 24; Mismatches 31; Indels 112; Gaps 2;

QY 6 ILLFLVAVATRVLSQVLQVQSGAEVVKPGASVKISKASGYTFTDTHAIHWYKQNPQGRLE 65
Db 7 IFSFLLISASVILLQVQSGSELKPKGASVKISKASGYTFTDYGNNWVKQAPGQGLK 66
QY 66 WIGYFSPGNDDFKNERFKGKATLTADTSASTAYVELSLRSEDTAYFCTRS--LNWAY 123
Db 67 WMGWINTYTGSTYVDDFKGRFVFLSDTSVSAAYLQISSLKAEDEATYFCARRGFYAMDY 126
QY 124 WGQGLTVTVSSASTKGPSVFLAPSSKSTSGTAAALGCLVKDYFPEPVTYVSWNSGALTSG 183
Db 127 WGQGLTVTVSSASTKGPSVFLAPSSKSTSGTAAALGCLVKDYFPEPVTYVSWNSGALTSG 186
QY 184 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKKEPKSCDKTHTC 243
Db 187 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKKEPKSCDKTHTC 246
QY 244 PPCP----- 247
Db 247 PPCPAPELLGGPSVFLFPPPKPDTLMISRTPEVTCVVDVDSHEDPEVKFNWYVDGVEVHN 306
QY 248 -----GPREP 253
Db 307 AKTAPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTIKAKGQPREP 366
QY 254 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLDSDGSFFL 313
Db 367 QVYTLPPSRDEMTKQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLDSDGSFFL 426
QY 314 YSKLTVDKSRWQQGNVFPSCSVMEALHNHYTQKSLSLSPGK 354
Db 427 YSKLTVDKSRWQQGNVFPSCSVMEALHNHYTQKSLSLSPGK 467

RESULT 8
US-09-485-737B-90


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; APPLICANT: CARRENO, BEATRIZ
; APPLICANT: CELNIKER, ABBIE CHERYL
; APPLICANT: COLLINS, MARY
; APPLICANT: GOLDMAN, SAMUEL
; APPLICANT: GRAY, GARY S.
; APPLICANT: KNIGHT, ANDREA
; APPLICANT: O'HARA, DENISE
; APPLICANT: RUP, BONITA
; APPLICANT: VELDMAN, GERTTRUIDA M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
; FILE REFERENCE: 08702.0081-01000
; CURRENT APPLICATION NUMBER: US/09/627,896B
; CURRENT FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 24
; TYPE: PRT
; ORGANISM: 3D1 heavy chain
; US-09-627-896B-24

Query Match          79.2%; Score 1485; DB 4; Length 462;
Best Local Similarity 63.9%; Pred. No. 3.7e-106;
Matches 297; Conservative 21; Mismatches 33; Indels 114; Gaps 4;

Qy 1 MGWSLLFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDHAHIVKQNP 60
Db 1 MGWCIIFLVTATGHSQVQLVQSGAEVVKPGSSVKVSKASGYTFTDVAIQVRQAP 60
Qy 61 GQRLWIGYFPGNDDFKYNRPFGKATLTADTSASTAYVELSLRSEDATVYFCTSL- 119
Db 61 GQGLWIGVINIYDNTYINQKFGKATMTVDKSTSTAYMELSLRSEDATVYICARA- 120
Qy 120 NMAYWGQGLTVTVSSASTKGPSVPLAPSSKSTSGTAAALGCLVKDYPPEVPTVSWNSGA 179
Db 121 YMDYWGQGLTVTVSSASTKGPSVPLAPSSKSTSGTAAALGCLVKDYPPEVPTVSWNSGA 180
Qy 180 LTSGVHTPPAVLQSSGLYSLSVTVPSSTSGTQYICNVNHNKPSNT-KVDKKEPKSCD 238
Db 181 LTSGVHTPPAVLQSSGLYSLSVTVPSSTSGTQYICNVNHNKPSNT-KVDKKEPKSCD 240
Qy 239 KTHICPPCP----- 247
Db 241 E---CPPCPAPPAAPSVFLPPPKOTLMISRTPEVTCVVVDVSHEDPEVQFNYYVDGV 297
Qy 248 -----GQ 249
Db 298 EVHNAKTPREQNSTFRVVSVLTVVHQMGLNGKEYKCKVSNKGLPAPIEKTISKTKGQ 357
Qy 250 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDG 309
Db 358 PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDG 417
Qy 310 SFFLYSKLTVDKSRWQGNVFSCSVMHALHNHYTKLSLSPGK 354
Db 418 SFFLYSKLTVDKSRWQGNVFSCSVMHALHNHYTKLSLSPGK 462

RESULT 13
US-08-487-550-8
; Sequence 8, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street

```

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; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,550
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-487-550-8

Query Match          79.2%; Score 1485; DB 3; Length 478;
Best Local Similarity 61.1%; Pred. No. 3.8e-106;
Matches 292; Conservative 25; Mismatches 37; Indels 124; Gaps 3;

Qy 1 MGWSLLFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDHAHIVKQNP 60
Db 1 MGWSLLFLVAVATRVQCEVQLVESGGLVQPGSLRVSCAVSGFTFSDHYMYFRQAP 60
Qy 61 GQRLWIGYF--SPGNDDFKYNRPFGKATLTADTSASTAYVELSLRSEDATVYFCTRS 118
Db 61 GKGPEWGFIRNRPNGGTTTAAASVKDRFTISRDDSKSIAYLQMSLSLKIEDTAVYCYTS 120
Qy 119 L-----NMAYWGQGLTVTVSSASTKGPSVPLAPSSKSTSGTAAALGCLVKDY 166
Db 121 YISHCRGVYCYGYFEPFGQGLVTVSSASTKGPSVPLAPSSKSTSGTAAALGCLVKDY 180
Qy 167 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSVTVPSSTSGTQYICNVNHNKPSNT 226
Db 181 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSVTVPSSTSGTQYICNVNHNKPSNT 240
Qy 227 KVDKKEPKSCDKTHTCPPCP----- 247
Db 241 KVDKKEPKSCDKTHTCPPCPAPPELLGGPSVFLPPPKPKOTLMISRTPEVTCVVVDVSH 300
Qy 248 ----- 247
Db 301 DPEVKFNWYVDGVEVHNAKTKPREEQNSTYRVVSVLTVLHQMGLNGKEYKCKVSNKALP 360
Qy 248 -----GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 296
Db 361 APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 420
Qy 297 NYKTTTPVLDSDGSFFLYSKLTVDKSRWQGNVFSCSVMHALHNHYTKLSLSPGK 354
Db 421 NYKTTTPVLDSDGSFFLYSKLTVDKSRWQGNVFSCSVMHALHNHYTKLSLSPGK 478

RESULT 14
US-09-526-098-8
; Sequence 8, Application US/09526098
; Patent No. 6492134
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,

```

;; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
;; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"

;; NUMBER OF SEQUENCES: 12
;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

;; STREET: 699 Prince Street

;; CITY: Alexandria

;; STATE: VA

;; COUNTRY: USA

;; ZIP: 22314

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: Patent In Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/526,098

;; FILING DATE:

;; CLASSIFICATION:

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: 09/383,916

;; FILING DATE:

;; APPLICATION NUMBER: US 08/487,550

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Teskin, Robin L.

;; REGISTRATION NUMBER: 35,030

;; REFERENCE/DOCKET NUMBER: 012712-131

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 703-836-6620

;; TELEFAX: 703-836-2021

;; INFORMATION FOR SEQ ID NO: 8:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 478 amino acids

;; TYPE: amino acid

;; TOPOLOGY: linear

;; MOLECULE TYPE: protein

;; US-09-526-098-8

Query Match 79.2%; Score 1485; DB 4; Length 478;

Best Local Similarity 61.1%; Pred. No. 3.8e-106;

Matches 292; Conservative 25; Mismatches 37; Indels 124; Gaps 3;

Qy 1 MGWSLLILFLVAVATRVLSQVQLVQSGAEVVKVPGASVKISKASGYTFTDHAHWKQNP 60

Db 1 MGWSLLILFLVAVATRVQCEVQLVESGGGLVQPGSLRVSCAVSGFTFSDHYMYWFRQAP 60

Qy 61 GQLEWIGYF--SPGNDDFKYNERFKGKATLTADTSASTAYVELSSLRSEDYAVYFCTRS 118

Db 61 GKGPEWVGFIIRNKPNGGTFEYAAASKDRFTISRDDSKSIAYLQWSSLKIEDYAVYCYCTS 120

Qy 119 L-----NMAYWGQGLTVTVSSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDY 166

Db 121 YISHCRGVCYGGYFQFEGWQGLVTVSSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDY 180

Qy 167 FPEPTVTSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQYIICNVNHPKPSNT 226

Db 181 FPEPTVTSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQYIICNVNHPKPSNT 240

Qy 227 KVDKKVPEKSCDKHTKCPCCP----- 247

Db 241 KVDKKAEPKSCDKHTKCPCCPAPPELLGGPSVFLPFPKPTLMISRTPEVTCVVVDVSHE 300

Qy 248 ----- 247

Db 301 DPEVKFNWYDGVFVHNKAKTPREQYNSTYRVSVSLTVLHQDWLNGKEYKCKVSNKALP 360

Qy 248 -----GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 296

Db 361 APIETKISKAGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 420

Qy 297 NYKTTTPVLDSDGFFLYSKLTVDKSRWQQGNFVSCSVMHAEALNHHYTKQSLSLSPGK 354

Db 421 NYKTTTPVLDSDGFFLYSKLTVDKSRWQQGNFVSCSVMHAEALNHHYTKQSLSLSPGK 478

RESULT 15

US-09-383-916-8

;; Sequence 8, Application US/09383916

;; Patent No. 6709654

;; GENERAL INFORMATION:

;; APPLICANT: Anderson, Dartell R.

;; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

;; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,

;; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

;; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"

;; NUMBER OF SEQUENCES: 12

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

;; STREET: 699 Prince Street

;; CITY: Alexandria

;; STATE: VA

;; COUNTRY: USA

;; ZIP: 22314

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: Patent In Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/383,916

;; FILING DATE: 26-AUG-1999

;; CLASSIFICATION:

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 08/487,550

;; FILING DATE: 07-JUN-1995

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Teskin, Robin L.

;; REGISTRATION NUMBER: 35,030

;; REFERENCE/DOCKET NUMBER: 012712-131

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 703-836-6620

;; TELEFAX: 703-836-2021

;; INFORMATION FOR SEQ ID NO: 8:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 478 amino acids

;; TYPE: amino acid

;; TOPOLOGY: linear

;; MOLECULE TYPE: protein

;; US-09-383-916-8

Query Match 79.2%; Score 1485; DB 4; Length 478;

Best Local Similarity 61.1%; Pred. No. 3.8e-106;

Matches 292; Conservative 25; Mismatches 37; Indels 124; Gaps 3;

Qy 1 MGWSLLILFLVAVATRVLSQVQLVQSGAEVVKVPGASVKISKASGYTFTDHAHWKQNP 60

Db 1 MGWSLLILFLVAVATRVQCEVQLVESGGGLVQPGSLRVSCAVSGFTFSDHYMYWFRQAP 60

Qy 61 GQLEWIGYF--SPGNDDFKYNERFKGKATLTADTSASTAYVELSSLRSEDYAVYFCTRS 118

Db 61 GKGPEWVGFIIRNKPNGGTFEYAAASKDRFTISRDDSKSIAYLQWSSLKIEDYAVYCYCTS 120

Qy 119 L-----NMAYWGQGLTVTVSSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDY 166

Db 121 YISHCRGVCYGGYFQFEGWQGLVTVSSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDY 180

Qy 167 FPEPTVTSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQYIICNVNHPKPSNT 226

Db 181 FPEPTVTSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQYIICNVNHPKPSNT 240

Qy 227 KVDKKVPEKSCDKHTKCPCCP----- 247

Db 241 KVDKKAEPKSCDKHTKCPCCPAPPELLGGPSVFLPFPKPTLMISRTPEVTCVVVDVSHE 300

Qy 248 ----- 247

Db	301	DPEVKFNWYVDGVEVHNAKTYPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP	360
Qy	248	-----GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN	296
Db	361	APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN	420
Qy	297	NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHENHNYTKQSLSPGK	354
Db	421	NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHENHNYTKQSLSPGK	478

Search completed: March 23, 2005, 18:35:50
 Job time : 39.3535 secs

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OM protein - protein search, using sw model

Run on: March 23, 2005, 18:26:57 ; Search time 109.061 Seconds
(without alignments)
1074.721 Million cell updates/sec

Title: US-10-058-069-7
Perfect score: 1876
Sequence: 1 MGWSLILFLVAVATRVLSQ.....MHEALHNHYTKLSLSPGK 354

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1613.5	86.0	731	9	US-09-825-012-46 Sequence 46, Appl
2	1613.5	86.0	741	9	US-09-825-012-55 Sequence 55, Appl
3	1608.5	85.7	729	9	US-09-825-012-52 Sequence 52, Appl
4	1608.5	85.7	739	9	US-09-825-012-61 Sequence 61, Appl
5	1603	85.4	470	14	US-10-216-484-89 Sequence 89, Appl
6	1603	85.4	470	14	US-10-384-933-89 Sequence 89, Appl
7	1602.5	85.4	730	9	US-09-825-012-49 Sequence 49, Appl
8	1602.5	85.4	740	9	US-09-825-012-58 Sequence 58, Appl
9	1595	85.0	470	14	US-10-216-484-143 Sequence 143, App
10	1595	85.0	470	14	US-10-384-933-143 Sequence 143, App
11	1593	84.9	470	14	US-10-216-484-145 Sequence 145, App
12	1593	84.9	470	14	US-10-384-933-145 Sequence 145, App
13	1592	84.9	470	14	US-10-216-484-117 Sequence 117, App

14	1592	84.9	470	14	US-10-216-484-147	Sequence 147, App
15	1592	84.9	470	14	US-10-384-933-117	Sequence 117, App
16	1592	84.9	470	14	US-10-384-933-147	Sequence 147, App
17	1579	84.2	470	14	US-10-216-484-157	Sequence 157, App
18	1579	84.2	470	14	US-10-384-933-157	Sequence 157, App
19	1565.5	83.4	467	14	US-10-171-452A-41	Sequence 41, Appl
20	1565.5	83.4	467	14	US-10-171-452A-47	Sequence 47, Appl
21	1565.5	83.4	467	14	US-10-171-452A-53	Sequence 53, Appl
22	1565.5	83.4	467	14	US-10-171-452A-59	Sequence 59, Appl
23	1565.5	83.4	467	15	US-10-353-708-41	Sequence 41, Appl
24	1565.5	83.4	467	15	US-10-353-708-47	Sequence 47, Appl
25	1565.5	83.4	467	15	US-10-353-708-53	Sequence 53, Appl
26	1565.5	83.4	467	15	US-10-353-708-59	Sequence 59, Appl
27	1565.5	83.4	467	16	US-10-731-984-7	Sequence 7, Appl
28	1565.5	83.4	467	16	US-10-731-984-15	Sequence 15, Appl
29	1565.5	83.4	467	16	US-10-731-984-23	Sequence 23, Appl
30	1565.5	83.4	467	16	US-10-731-984-31	Sequence 31, Appl
31	1559.5	83.1	448	15	US-10-378-567-2	Sequence 2, Appl
32	1559	82.6	472	9	US-09-301-593-43	Sequence 43, Appl
33	1549	82.6	472	14	US-10-159-006-43	Sequence 43, Appl
34	1549	82.6	472	14	US-10-822-300-119	Sequence 119, App
35	1546.5	82.4	446	17	US-10-822-300-120	Sequence 120, App
36	1546.5	82.4	476	9	US-09-747-669-3	Sequence 3, Appl
37	1546	82.4	476	14	US-10-290-703-3	Sequence 3, Appl
38	1545.5	82.4	465	15	US-10-404-724-25	Sequence 25, Appl
39	1545.5	82.4	465	17	US-10-816-276-21	Sequence 21, Appl
40	1543.5	82.3	446	17	US-10-822-300-121	Sequence 121, App
41	1543.5	82.3	446	17	US-10-822-300-122	Sequence 122, App
42	1543.5	82.3	448	14	US-10-171-452A-42	Sequence 42, Appl
43	1543.5	82.3	448	14	US-10-171-452A-48	Sequence 48, Appl
44	1543.5	82.3	448	14	US-10-171-452A-54	Sequence 54, Appl
45	1543.5	82.3	448	14	US-10-171-452A-54	Sequence 54, Appl

ALIGNMENTS

RESULT 1
US-09-825-012-46
; Sequence 46, Application US/09825012
; Patent No. US20020122798A1
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-256808
; CURRENT APPLICATION NUMBER: US/09/825.012
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/237,159
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: GB 0008049.9
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
; LENGTH: 731
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised HMFG1 heavy chain - DNase I fusion
US-09-825-012-46

Query Match	86.0%;	Score 1613.5;	DB 9;	Length 731;
Best Local Similarity	67.7%;	Pred. No. 1.3e+101;		
Matches 316;	Conservative 18;	Mismatches 20;	Indels 113;	Gaps 2;
Oy	1	MGWSLILFLVAVATRVLSQVQSGAEVVKPGASVKISKASGYTFTDRAIHWKQNP	60	
Db	1	MGWSLILFLVATATGHSQVQVQSGAEVVKPGASVKISKASGYTTSAYWIEWRQAP	60	
Oy	61	QORLEWIGYFSGNDDFKYNERFKGKATLTADTSGASTAYVELSLRSDDTAVYFCTRSIN	120	
Db	61	CKGLEWGEIILPGSNNSYNEKFKGRVTVTDTSTNTAYMELSLRSDDTAVYCARSD	120	

Qy 121 ---MAYWQGGTLVTVSSASTKPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS 177
Db 121 FAWFAYWQGGTLVTVSSASTKPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS 180
Qy 178 GALTSGVHTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSC 237
Db 181 GALTSGVHTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSC 240
Qy 238 DKHTCTCPCP----- 247
Db 241 DKHTCTCPAPPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 300
Qy 248 ----- 247
Db 301 GVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 360
Qy 248 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 307
Db 361 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 420
Qy 308 DGSFFLYSKLTVDKSRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 354
Db 421 DGSFFLYSKLTVDKSRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 467

RESULT 2

US-09-825-012-55
; Sequence 55, Application US/09825012
; Patent No. US20020122798A1
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-256808
; CURRENT APPLICATION NUMBER: US/09/825,012
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/237,159
; PRIOR FILING DATE: 2000-10-02
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 55
; LENGTH: 741
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised HMFG1 heavy chain - DNase I fusion
US-09-825-012-55

Query Match 86.0%; Score 1613.5; DB 9; Length 741;
Best Local Similarity 67.7%; Pred. No. 1.4e-101;
Matches 316; Conservative 18; Mismatches 20; Indels 113; Gaps 2;
Qy 1 MGWSLILFLVAVATRVLSQVLVQSGAEVVKPGASVKISKASGYTFTDHAHHVKNQNP 60
Db 1 MGWSLILFLVATATGVHSQVLVQSGAEVVKPGASVKISKASGYTFTDHAHHVKNQNP 60
Qy 61 GQRLWIGYFSGNDPDKYNERFKGATLTADTSASTAYVELSLRSEDVAVYFCTSLN 120
Db 61 GKGLEWVGEIILPGSNRYNEKFKGRVTVTRDTSTNTAYMELSLRSEDVAVYFCTSLN 120
Qy 121 ---MAYWQGGTLVTVSSASTKPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS 177
Db 121 FAWFAYWQGGTLVTVSSASTKPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS 180
Qy 178 GALTSGVHTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSC 237
Db 181 GALTSGVHTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSC 240
Qy 238 DKHTCTCPCP----- 247
Db 241 DKHTCTCPAPPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 300
Qy 248 ----- 247
Db 301 GVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 360
Qy 248 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 307
Db 181 GALTSGVHTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSC 240
Qy 238 DKHTCTCPCP----- 247
Db 241 DKHTCTCPAPPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 300

Qy 248 ----- 247
Db 301 GVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 360
Qy 248 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 307
Db 361 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 420
Qy 308 DGSFFLYSKLTVDKSRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 354
Db 421 DGSFFLYSKLTVDKSRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 467

RESULT 3
US-09-825-012-52
; Sequence 52, Application US/09825012
; Patent No. US20020122798A1
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-256808
; CURRENT APPLICATION NUMBER: US/09/825,012
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/237,159
; PRIOR FILING DATE: 2000-10-02
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 52
; LENGTH: 729
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised HMFG1 heavy chain - DNase I fusion
US-09-825-012-52

Query Match 85.7%; Score 1608.5; DB 9; Length 729;
Best Local Similarity 67.6%; Pred. No. 2.9e-101;
Matches 315; Conservative 18; Mismatches 20; Indels 113; Gaps 2;
Qy 1 MGWSLILFLVAVATRVLSQVLVQSGAEVVKPGASVKISKASGYTFTDHAHHVKNQNP 60
Db 1 MGWSLILFLVATATGVHSQVLVQSGAEVVKPGASVKISKASGYTFTDHAHHVKNQNP 60
Qy 61 GQRLWIGYFSGNDPDKYNERFKGATLTADTSASTAYVELSLRSEDVAVYFCTSLN 120
Db 61 GKGLEWVGEIILPGSNRYNEKFKGRVTVTRDTSTNTAYMELSLRSEDVAVYFCTSLN 120
Qy 121 ---MAYWQGGTLVTVSSASTKPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS 177
Db 121 FAWFAYWQGGTLVTVSSASTKPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNS 180
Qy 178 GALTSGVHTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSC 237
Db 181 GALTSGVHTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSC 240
Qy 238 DKHTCTCPCP----- 247
Db 241 DKHTCTCPAPPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 300
Qy 248 ----- 247
Db 301 GVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 360
Qy 248 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 307
Db 361 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 420
Qy 308 DGSFFLYSKLTVDKSRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 353
Db 421 DGSFFLYSKLTVDKSRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 466

RESULT 4

US-09-825-012-61
; Sequence 61, Application US/09825012
; Patent No. US20020122798A1

GENERAL INFORMATION:

; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-258808
; CURRENT APPLICATION NUMBER: US/09/825,012
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/237,159
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: GB 0008049.9
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1

SEQ ID NO 61

LENGTH: 739

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

; OTHER INFORMATION: Humanised HMFG1 heavy chain - DNase I fusion
US-09-825-012-61

Query Match 85.7%; Score 1608.5; DB 9; Length 739;
Best Local Similarity 67.6%; Pred. No. 3e-101;
Matches 315; Conservative 18; Mismatches 20; Indels 113; Gaps 2;

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Qy 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFDTHAIHWKQNP 60
Db 1 MGWSLILFLVATATGVHSQVQLVQSGAEVVKPGASVKISKASGYTFSAIHWKQNP 60

Qy 61 GORLEWIGYFPGNDDFKYNRPFKQKATLTADTASTAYVELSLRSEDYAVFCTRLN 120
Db 61 GKLEWVGEILPGSNNSRYNEKFGKRVTVTRDTSTNTAYMELSLRSEDYAVYCARSD 120

Qy 121 ---MAYQGQGLTVTVSSASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPTVSWNS 177
Db 121 FAWFAYMGQGLTVTVSSASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPTVSWNS 180

Qy 178 GALTSGVHTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNKKPSNTKVDKVEPKSC 237
Db 181 GALTSGVHTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNKKPSNTKVDKVEPKSC 240

Qy 238 DKHTCTPCPP----- 247
Db 241 DKHTCTPCPPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVD 300

Qy 248 ----- 247
Db 301 GVEVHNAKTKPREQYNSTYRVSVLVTLVHQDWLNGKEYCKCKVSNKALPAPIEKTISKAK 360

Qy 248 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 307
Db 361 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 420

Qy 308 DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSPG 353
Db 421 DGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSPG 466
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RESULT 5

US-10-216-484-89
; Sequence 89, Application US/10216484
; Publication No. US20030103976A1

GENERAL INFORMATION:

; APPLICANT: Serizawa, No. US20030103976Alufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies

FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/216,484
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 89
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Designed heavy
; OTHER INFORMATION: chain of humanized anti-Fas antibody
US-10-216-484-89

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Query Match 85.4%; Score 1603; DB 14; Length 470;
Best Local Similarity 67.0%; Pred. No. 4.2e-101;
Matches 315; Conservative 17; Mismatches 22; Indels 116; Gaps 2;

Qy 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFDTHAIHWKQNP 60
Db 1 MGWSLILFLVATATGVHSQVQLVQSGAEVVKPGASVKISKASGYTFSTYMMQWVKQAP 60

Qy 61 GORLEWIGYFPGNDDFKYNRPFKQKATLTADTASTAYVELSLRSEDYAVFCTRLN 120
Db 61 GORLEWIGYFPGNDDFKYNRPFKQKATLTADTASTAYVELSLRSEDYAVYCARNRD 120

Qy 121 MA-----YMQGQGLTVTVSSASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPTVTS 174
Db 121 YSNWYFDMWEGGLTVTVSSASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPTVTS 180

Qy 175 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNKKPSNTKVDKVEPK 234
Db 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNKKPSNTKVDKVEPK 240

Qy 235 KSCDKHTCTPCPP----- 247
Db 241 KSCDKHTCTPCPPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW 300

Qy 248 ----- 247
Db 301 YVDGVEVHNAKTKPREQYNSTYRVSVLVTLVHQDWLNGKEYCKCKVSNKALPAPIEKTIS 360

Qy 248 ---GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 304
Db 361 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 420

Qy 305 LDSGSPFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSPGK 354
Db 421 LDSGSPFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKLSLSPGK 470
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RESULT 6

US-10-384-933-89

; Sequence 89, Application US/10384933

; Publication No. US20030170817A1

GENERAL INFORMATION:

; APPLICANT: Serizawa, No. US20030170817Alufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/384,933
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165

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; SEQ ID NO 89
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Designed heavy
; OTHER INFORMATION: chain of humanized anti-Fas antibody
US-10-384-933-89

Query Match      85.4%; Score 1603; DB 14; Length 470;
Best Local Similarity 67.0%; Pred. No. 4.2e-101;
Matches 315; Conservative 17; Mismatches 22; Indels 116; Gaps 2;

Qy 1 MGWSLILLFLVAVATRVLSQVQSGAEVVKPGASVKISKASGYTFTDHAHHWKQNP 60
Db 1 MGWSLILLFLVAVATRVLSQVQSGAEVVKPGASVKISKASGYTFTDHAHHWKQNP 60

Qy 61 GQRLWIGYFSPGNDDFKYNRERKFKATLTADTASATAYVELSLRSEDVAVYFCTSLN 120
Db 61 GQRLWIGYFSPGNDDFKYNRERKFKATLTADTASATAYVELSLRSEDVAVYFCTSLN 120

Qy 121 MA-----YMGQGLTVTVSSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYRPEPTVS 174
Db 121 YSNWYFDVWEGGLTVTVSSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYRPEPTVS 180

Qy 175 WNSGALTSQVHTFPFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKKEVP 234
Db 181 WNSGALTSQVHTFPFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKKEVP 240

Qy 235 KSCDKTHTCPPCP----- 247
Db 241 KSCDKTHTCPPCPAPPELLGSPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300

Qy 248 ----- 247
Db 301 YVDGVEVNAKTPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIIS 360

Qy 248 ---GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 304
Db 361 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 420

Qy 305 LDSGSPFLYSLKLTVDKSRWQOGNPFVSCSVHMEALHNNHYTKSLSPGK 354
Db 421 LDSGSPFLYSLKLTVDKSRWQOGNPFVSCSVHMEALHNNHYTKSLSPGK 470

RESULT 7
US-09-825-012-49
; Sequence 49, Application US/09825012
; Patent No. US20020122798A1
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-256808
; CURRENT APPLICATION NUMBER: US/09/825,012
; CURRENT FILING DATE: 2001-04-03
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: GB 0008049.9
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 49
; LENGTH: 730
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised HMFG1 heavy chain - DNase I fusion
US-09-825-012-49

Query Match      85.4%; Score 1602.5; DB 9; Length 730;
Best Local Similarity 67.5%; Pred. No. 7.5e-101;
Matches 314; Conservative 18; Mismatches 20; Indels 113; Gaps 2;

Qy 1 MGWSLILLFLVAVATRVLSQVQSGAEVVKPGASVKISKASGYTFTDHAHHWKQNP 60
Db 1 MGWSLILLFLVAVATRVLSQVQSGAEVVKPGASVKISKASGYTFTDHAHHWKQNP 60

Qy 61 GQRLWIGYFSPGNDDFKYNRERKFKATLTADTASATAYVELSLRSEDVAVYFCTSLN 120
Db 61 GQRLWIGYFSPGNDDFKYNRERKFKATLTADTASATAYVELSLRSEDVAVYFCTSLN 120

Qy 121 MA-----YMGQGLTVTVSSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYRPEPTVS 174
Db 121 YSNWYFDVWEGGLTVTVSSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYRPEPTVS 180

Qy 175 WNSGALTSQVHTFPFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKKEVP 234
Db 181 WNSGALTSQVHTFPFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKKEVP 240

Qy 235 KSCDKTHTCPPCP----- 247
Db 241 KSCDKTHTCPPCPAPPELLGSPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300

Qy 248 ----- 247
Db 301 YVDGVEVNAKTPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIIS 360

Qy 248 ---GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 304
Db 361 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 420

Qy 305 LDSGSPFLYSLKLTVDKSRWQOGNPFVSCSVHMEALHNNHYTKSLSPGK 354
Db 421 LDSGSPFLYSLKLTVDKSRWQOGNPFVSCSVHMEALHNNHYTKSLSPGK 470

RESULT 8
US-09-825-012-58
; Sequence 58, Application US/09825012
; Patent No. US20020122798A1
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-256808
; CURRENT APPLICATION NUMBER: US/09/825,012
; CURRENT FILING DATE: 2001-04-03
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: GB 0008049.9
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 58
; LENGTH: 740
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised HMFG1 heavy chain - DNase I fusion
US-09-825-012-58

Query Match      85.4%; Score 1602.5; DB 9; Length 740;
Best Local Similarity 67.5%; Pred. No. 7.6e-101;
Matches 314; Conservative 18; Mismatches 20; Indels 113; Gaps 2;

Qy 1 MGWSLILLFLVAVATRVLSQVQSGAEVVKPGASVKISKASGYTFTDHAHHWKQNP 60
Db 1 MGWSLILLFLVAVATRVLSQVQSGAEVVKPGASVKISKASGYTFTDHAHHWKQNP 60

Qy 61 GQRLWIGYFSPGNDDFKYNRERKFKATLTADTASATAYVELSLRSEDVAVYFCTSLN 120
Db 61 GQRLWIGYFSPGNDDFKYNRERKFKATLTADTASATAYVELSLRSEDVAVYFCTSLN 120

Qy 121 MA-----YMGQGLTVTVSSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYRPEPTVS 174
Db 121 YSNWYFDVWEGGLTVTVSSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYRPEPTVS 180

Qy 175 WNSGALTSQVHTFPFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKKEVP 234
Db 181 WNSGALTSQVHTFPFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKKEVP 240

Qy 235 KSCDKTHTCPPCP----- 247
Db 241 KSCDKTHTCPPCPAPPELLGSPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300

Qy 248 ----- 247
Db 301 YVDGVEVNAKTPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIIS 360

Qy 248 ---GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 304
Db 361 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 420

Qy 305 LDSGSPFLYSLKLTVDKSRWQOGNPFVSCSVHMEALHNNHYTKSLSPGK 354
Db 421 LDSGSPFLYSLKLTVDKSRWQOGNPFVSCSVHMEALHNNHYTKSLSPGK 470

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Qy 178 GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHPKNTKVDKKVEPKSC 237
Db 181 GALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHPKNTKVDKKVEPKSC 240
Qy 238 DKTHTCPPCP----- 247
Db 241 DKTHTCPPCPAPELLGGPSVFLPPPKDITLMSRTPEVTVVVDVSHEDPEVKFNWVD 300
Qy 248 ----- 247
Db 301 GVEVHNAKTPREEQYNSTYRVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKAK 360
Qy 248 GQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEVNESGQPNNTKTTTPVLD 307
Db 361 GQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEVNESGQPNNTKTTTPVLD 420
Qy 308 DGSFPLYSLKLTVDKSRWQGNVFCVSNVHEALHNHYTKQSLSLSP 352
Db 421 DGSFPLYSLKLTVDKSRWQGNVFCVSNVHEALHNHYTKQSLSLSP 465
RESULT 9
US-10-216-484-143
; Sequence 143, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030103976A1ufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/216,484
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 143
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Designed heavy
; OTHER INFORMATION: chain of humanized anti-Fas antibody
US-10-216-484-143

Query Match 85.0%; Score 1595; DB 14; Length 470;
Best Local Similarity 66.8%; Pred. No. 1.5e-100;
Matches 314; Conservative 16; Mismatches 24; Indels 116; Gaps 2;
Qy 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDHAHVKQNP 60
Db 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDHAHVKQNP 60
Qy 61 GQLEWIGYFSPGNDPFKYNRFRFGKATLTADTASTAYVELSLRSSEDTAVYFCTRLN 120
Db 61 GQLEWIGYFSPGNDPFKYNRFRFGKATLTADTASTAYVELSLRSSEDTAVYFCTRLN 120
Qy 121 MA-----YWGQGLTVTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTV 174
Db 121 YSNWYFDVWGQGLTVTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTV 180
Qy 175 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHPKNTKVDKKVEP 234
Db 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHPKNTKVDKKVEP 240
Qy 235 KSCDKHTCTCPCP----- 247
Db 241 KSCDKHTCTCPCPAPELLGGPSVFLPPPKDITLMSRTPEVTVVVDVSHEDPEVKFNW 300
Qy 301 GVEVHNAKTPREEQYNSTYRVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKAK 360
Qy 248 ---GQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEVNESGQPNNTKTTTPV 304
Db 361 KAKGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEVNESGQPNNTKTTTPV 420

Qy 248 ----- 247
Db 301 YVDGVEVHNAKTPREEQYNSTYRVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKTIS 360
Qy 248 ---GQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEVNESGQPNNTKTTTPV 304
Db 361 KAKGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEVNESGQPNNTKTTTPV 420
Qy 305 LDSGSPFLYSLKLTVDKSRWQGNVFCVSNVHEALHNHYTKQSLSLSPGK 354
Db 421 LDSGSPFLYSLKLTVDKSRWQGNVFCVSNVHEALHNHYTKQSLSLSPGK 470
RESULT 10
US-10-384-933-143
; Sequence 143, Application US/10384933
; Publication No. US20030170817A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030170817A1ufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/384,933
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 143
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Designed heavy
; OTHER INFORMATION: chain of humanized anti-Fas antibody
US-10-384-933-143

Query Match 85.0%; Score 1595; DB 14; Length 470;
Best Local Similarity 66.8%; Pred. No. 1.5e-100;
Matches 314; Conservative 16; Mismatches 24; Indels 116; Gaps 2;
Qy 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDHAHVKQNP 60
Db 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTSYMMQVQKAP 60
Qy 61 GQLEWIGYFSPGNDPFKYNRFRFGKATLTADTASTAYVELSLRSSEDTAVYFCTRLN 120
Db 61 GQLEWIGYFSPGNDPFKYNRFRFGKATLTADTASTAYVELSLRSSEDTAVYFCTRLN 120
Qy 121 MA-----YWGQGLTVTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTV 174
Db 121 YSNWYFDVWGQGLTVTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTV 180
Qy 175 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHPKNTKVDKKVEP 234
Db 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHPKNTKVDKKVEP 240
Qy 235 KSCDKHTCTCPCP----- 247
Db 241 KSCDKHTCTCPCPAPELLGGPSVFLPPPKDITLMSRTPEVTVVVDVSHEDPEVKFNW 300
Qy 248 ----- 247
Db 301 YVDGVEVHNAKTPREEQYNSTYRVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKTIS 360
Qy 248 ---GQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEVNESGQPNNTKTTTPV 304
Db 361 KAKGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEVNESGQPNNTKTTTPV 420

Qy 305 LDSGSPFLYKLTVDKSRWQGNVFCVSMHEALHNNHYTKSLSPGK 354
 Db 421 LDSGSPFLYKLTVDKSRWQGNVFCVSMHEALHNNHYTKSLSPGK 470

RESULT 11

US-10-216-484-145
 ; Sequence 145, Application US/10216484
 ; Publication No. US20030103976A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Serizawa, No. US20030103976A1ufusa
 ; APPLICANT: Haruyama, Hideyuki
 ; APPLICANT: Nakahara, Kaori
 ; APPLICANT: Tamaki, Ikuko
 ; APPLICANT: Takahashi, Tohru
 ; TITLE OF INVENTION: Anti-Fas Antibodies
 ; FILE REFERENCE: 980126CIP/HG
 ; CURRENT APPLICATION NUMBER: US/10/216,484
 ; PRIOR FILING DATE: 2002-08-09
 ; PRIOR APPLICATION NUMBER: US/09/499,662
 ; PRIOR FILING DATE: 2000-02-09
 ; PRIOR APPLICATION NUMBER: US 09/053,583
 ; PRIOR FILING DATE: 1998-04-01
 ; NUMBER OF SEQ ID NOS: 165
 ; SEQ ID NO 145
 ; LENGTH: 470
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Designed heavy
 ; OTHER INFORMATION: chain of humanized anti-Fas antibody
 US-10-216-484-145

Query Match 84.9%; Score 1593; DB 14; Length 470;
 Best Local Similarity 66.6%; Pred. No. 2e-100;

Matches 313; Conservative 17; Mismatches 24; Indels 116; Gaps 2;

Qy 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDHAHWKQNP 60
 Db 1 MGWSLILFLVATATGVSQVQLVQSGAEVVKPGASVKISKASGYTFTSVMQWVKQAP 60
 Qy 61 GQRLWIGYFSGNDDFKYNRPFKGAATLTADTSASTAYVELSLRSEDVAVYCTRLN 120
 Db 61 GQGLWNGEIDPSDSTYNYNQKFGKATITVDSTSTAYMELSLRSEDVAVYCARND 120
 Qy 121 MA-----YMGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVS 174
 Db 121 YSNWYFDWQGLTVTVSSASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVS 180
 Qy 175 WNSGALTSQVHTTFAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKKVEP 234
 Db 181 WNSGALTSQVHTTFAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKKVEP 240
 Qy 235 KSCDKHTCTCPCP----- 247
 Db 241 KSCDKHTCTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
 Qy 248 ----- 247
 Db 301 YVDGVEVHNAKTPREQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
 Qy 248 ---GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 304
 Db 361 KAKGQPREPQVYTLPPSRDEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 420
 Qy 305 LDSGSPFLYKLTVDKSRWQGNVFCVSMHEALHNNHYTKSLSPGK 354
 Db 421 LDSGSPFLYKLTVDKSRWQGNVFCVSMHEALHNNHYTKSLSPGK 470

RESULT 12

US-10-384-933-145

; Sequence 145, Application US/10384933
 ; Publication No. US200301070817A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Serizawa, No. US200301070817A1ufusa
 ; APPLICANT: Haruyama, Hideyuki
 ; APPLICANT: Nakahara, Kaori
 ; APPLICANT: Tamaki, Ikuko
 ; APPLICANT: Takahashi, Tohru
 ; TITLE OF INVENTION: Anti-Fas Antibodies
 ; FILE REFERENCE: 980126CIP/HG
 ; CURRENT APPLICATION NUMBER: US/10/384,933
 ; PRIOR FILING DATE: 2003-02-05
 ; PRIOR APPLICATION NUMBER: US/09/499,662
 ; PRIOR FILING DATE: 2000-02-09
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01
 ; NUMBER OF SEQ ID NOS: 165
 ; SEQ ID NO 145
 ; LENGTH: 470
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Designed heavy
 ; OTHER INFORMATION: chain of humanized anti-Fas antibody
 US-10-384-933-145

Query Match 84.9%; Score 1593; DB 14; Length 470;
 Best Local Similarity 66.6%; Pred. No. 2e-100;
 Matches 313; Conservative 17; Mismatches 24; Indels 116; Gaps 2;
 Qy 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDHAHWKQNP 60
 Db 1 MGWSLILFLVATATGVSQVQLVQSGAEVVKPGASVKISKASGYTFTSVMQWVKQAP 60
 Qy 61 GQRLWIGYFSGNDDFKYNRPFKGAATLTADTSASTAYVELSLRSEDVAVYCTRLN 120
 Db 61 GQGLWNGEIDPSDSTYNYNQKFGKATITVDSTSTAYMELSLRSEDVAVYCARND 120
 Qy 121 MA-----YMGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVS 174
 Db 121 YSNWYFDWQGLTVTVSSASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVS 180
 Qy 175 WNSGALTSQVHTTFAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKKVEP 234
 Db 181 WNSGALTSQVHTTFAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKKVEP 240
 Qy 235 KSCDKHTCTCPCP----- 247
 Db 241 KSCDKHTCTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
 Qy 248 ----- 247
 Db 301 YVDGVEVHNAKTPREQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
 Qy 248 ---GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 304
 Db 361 KAKGQPREPQVYTLPPSRDEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 420
 Qy 305 LDSGSPFLYKLTVDKSRWQGNVFCVSMHEALHNNHYTKSLSPGK 354
 Db 421 LDSGSPFLYKLTVDKSRWQGNVFCVSMHEALHNNHYTKSLSPGK 470

RESULT 13

US-10-216-484-117
 ; Sequence 117, Application US/10216484
 ; Publication No. US20030103976A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Serizawa, No. US20030103976A1ufusa
 ; APPLICANT: Haruyama, Hideyuki
 ; APPLICANT: Nakahara, Kaori
 ; APPLICANT: Tamaki, Ikuko
 ; APPLICANT: Takahashi, Tohru

```
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/216,484
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 117
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Designed heavy
; OTHER INFORMATION: chain of humanized anti-Fas antibody
US-10-216-484-117

Query Match      84.9%; Score 1592; DB 14; Length 470;
Best Local Similarity 66.6%; Pred. No. 2.4e-100;
Matches 313; Conservative 17; Mismatches 24; Indels 116; Gaps 2;

QY 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDHAHWKQNP 60
DB 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDHAHWKQNP 60
QY 61 GORLEWIGYFSPGNDDFKYNRFKPKATLTADTASTAYVELSLRSSEDTAVYFCTRSIN 120
DB 61 GORLEWIGYFSPGNDDFKYNRFKPKATLTADTASTAYVELSLRSSEDTAVYFCTRSIN 120
QY 121 MA-----YMGQGTLTAVTSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPTVTS 174
DB 121 YSNWYFDMVQEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPTVTS 180
QY 175 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHHKPSNTKVDKVEP 234
DB 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHHKPSNTKVDKVEP 240
QY 235 KSCDKHTCTCPCP----- 247
DB 241 KSCDKHTCTCPCPPELLGSPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
QY 248 ----- 247
DB 301 YVDGVEVHNATKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
QY 248 ---GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 304
DB 361 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 420
QY 305 LDSGSPFLYSLKLTVDKSRWQGNVFCSCVMHEALHNNHYTKSLSPGK 354
DB 421 LDSGSPFLYSLKLTVDKSRWQGNVFCSCVMHEALHNNHYTKSLSPGK 470

RESULT 14
US-10-216-484-147
; Sequence 147, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030103976A1ufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/216,484
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 117
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Designed heavy
; OTHER INFORMATION: chain of humanized anti-Fas antibody
US-10-216-484-117

Query Match      84.9%; Score 1592; DB 14; Length 470;
Best Local Similarity 66.6%; Pred. No. 2.4e-100;
Matches 313; Conservative 17; Mismatches 24; Indels 116; Gaps 2;

QY 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDHAHWKQNP 60
DB 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDHAHWKQNP 60
QY 61 GORLEWIGYFSPGNDDFKYNRFKPKATLTADTASTAYVELSLRSSEDTAVYFCTRSIN 120
DB 61 GORLEWIGYFSPGNDDFKYNRFKPKATLTADTASTAYVELSLRSSEDTAVYFCTRSIN 120
QY 121 MA-----YMGQGTLTAVTSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPTVTS 174
DB 121 YSNWYFDMVQEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPTVTS 180
QY 175 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHHKPSNTKVDKVEP 234
DB 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHHKPSNTKVDKVEP 240
QY 235 KSCDKHTCTCPCP----- 247
DB 241 KSCDKHTCTCPCPPELLGSPSVFLPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
QY 248 ----- 247
DB 301 YVDGVEVHNATKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
QY 248 ---GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 304
DB 361 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 420
QY 305 LDSGSPFLYSLKLTVDKSRWQGNVFCSCVMHEALHNNHYTKSLSPGK 354
DB 421 LDSGSPFLYSLKLTVDKSRWQGNVFCSCVMHEALHNNHYTKSLSPGK 470

RESULT 15
US-10-384-933-117
; Sequence 117, Application US/10384933
; Publication No. US20030170817A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030170817A1ufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/384,933
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 117
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Designed heavy
; OTHER INFORMATION: chain of humanized anti-Fas antibody
US-10-384-933-117
```

US-10-384-933-117

```

Query Match      84.9%; Score 1592; DB 14; Length 470;
Best Local Similarity 66.6%; Pred. No. 2.4e-100;
Matches 313; Conservative 17; Mismatches 24; Indels 116; Gaps 2;

Qy 1 MGWSLILLFLVAVATRVLSQVLVQSGAEVVKPGASVKISKASGYFTDHAHHVKNP 60
Db 1 MGWSLILLFLVAVATRVLSQVLVQSGAEVVKPGASVKISKASGYFTDHAHHVKNP 60
Qy 61 GQLEWIGYFSPGNDPFKYNRFKGAATLTADTSATYAYVELSLRSEDVAVYFCTSLN 120
Db 61 GQLEWIGYFSPGNDPFKYNRFKGAATLTADTSATYAYVELSLRSEDVAVYFCTSLN 120
Qy 121 MA-----YMQGTLVTYSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVS 174
Db 121 YSNNWYFDVWGEGTLVTYSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVS 180
Qy 175 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNNHKPSNTKVDKVEP 234
Db 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNNHKPSNTKVDKVEP 240
Qy 235 KSCDKTHCTCPPCP----- 247
Db 241 KSCDKTHCTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
Qy 248 ----- 247
Db 301 YVDGVEVHNAKTPREEQYNSTYRVSVLTVTLHQDLNLNGKEYCKVSNKALPAPIEKTIS 360
Qy 248 ---GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPV 304
Db 361 KAGQPREPQVYTLPPSRDEMTKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPV 420
Qy 305 LDSGSPFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTOKSLSPGK 354
Db 421 LDSGSPFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTOKSLSPGK 470

```

Search completed: March 23, 2005, 18:40:00
Job time : 112.061 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: March 23, 2005, 18:12:06 ; Search time 32.7778 Seconds
(without alignments)
1039.141 Million cell updates/sec

Title: US-10-058-069-7
Perfect score: 1876
Sequence: 1 MGWSLILFLVAVATRVLSQ.....MHEALHNHYTKQSLSLSPGK 354
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1127.5	60.1	469	2 S37483	Ig gamma-2a chain
2	1116	59.5	330	1 GHU	Ig gamma-1 chain C
3	1094	58.3	446	2 S40295	Ig gamma-2a chain
4	1066	56.8	474	1 G2MS11	Ig gamma-2b chain
5	1030.5	54.9	475	2 S01321	Ig gamma-2b chain
6	1006	53.6	326	1 G2HU	Ig gamma-2 chain C
7	997.5	53.2	377	2 A23511	Ig gamma-3 chain C
8	995.5	53.1	377	2 A60764	Ig gamma-3 chain C
9	981.5	52.3	444	2 PC4436	monoclonal antibod
10	974.5	51.9	327	1 G4HU	Ig gamma-4 chain C
11	946	50.4	470	2 S22080	Ig heavy chain pre
12	940	50.1	472	2 S31459	Ig gamma-1 chain -
13	852	45.4	374	2 S69339	Ig heavy chain V r
14	814.5	43.4	241	2 S69131	Ig heavy chain (DO
15	809	43.1	246	2 S38950	Ig gamma chain - m
16	803.5	42.8	249	2 S69340	Ig heavy chain VHI
17	777	41.4	220	2 A49444	Ig gamma-1 heavy c
18	769	41.0	548	2 S38864	Ig epsilon chain C
19	748	39.9	218	2 A36040	Ig heavy chain V-I
20	737	39.3	328	2 I47159	Ig gamma 2a chain
21	733	39.1	328	2 I47158	Ig gamma 1 chain c
22	732	39.0	328	2 I47161	Ig gamma 3 chain c
23	731	39.0	328	2 I47160	Ig gamma 2b chain
24	726	38.7	214	2 PC4202	monoclonal antibod
25	722.5	38.5	323	1 GHRB	Ig gamma chain C r
26	722	38.5	322	2 PS0019	Ig gamma-2a chain
27	720	38.4	326	2 PS0017	Ig gamma-1 chain C
28	715.5	38.1	221	2 S49220	Ig gamma-1 chain -
29	707	37.7	549	2 S04845	Ig heavy chain pre

RESULT 1
S37483
Ig gamma-2a chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37483
R:Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A:Reference number: S37483
A:Accession: S37483
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-469 <DUC>
A:Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
P:276-345/Domain: immunoglobulin homology <IMM>

Query Match	60.1%	Score	1127.5	DB 2	Length	469			
Best Local Similarity	48.2%	Pred. No.	1.2e-60						
Matches	227	Conservative	45	Mismatches	80	Indels	119	Gaps	4
Qy	1	MGWSLILFLVAVATRVLSQVLVQSGAEVVKPGASVKISKASGYTFTDHALHWKQP	60						
Db	1	MGWSWIFLLSLGSGTAGVHCQIQQQGPELVKPGASVKISKASGYTFTDYINWVKQP	60						
Qy	61	GQRLWIGYFSPGNDDFKYNERFGKATLTADTGASTAYVELSLRSDTAVYFCTRSIN	120						
Db	61	GQGLKWIWYIPASGNTKYNENFKGATLTVDTSSTAYMQLSSLTSDTAVYFCARANG	120						
Qy	121	-----MAYWGQGLTVTVSSASTKGPSVPPLAPSKSTSGGTAALGCLVKDYFPEPTVSW	175						
Db	121	ATATLLDWYGQGLTVTVSSAKTTAPSVVPLAPVCGDTTSGSVTLGCLVKGYFPEPTLTW	180						
Qy	176	NSGALTSGVHTFPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHHKPSNTKVDKVPK	235						
Db	181	NSGSLSSGVHTFPAVLQSD-LYTLSSSVTVTSSTWPSQSIITCNVAHPASSTKVDKIEPR	239						
Qy	236	SCDKTHTCPPC-----	246						
Db	240	G-PTIKPCPECKCPAPNLLGGPSVIFPPPKIKDVLMSLSPIVTCVVVDSEDDPDVQIS	298						
Qy	247	-----	246						
Db	299	WFVNVNVEHTAQTHREDYNSLTRVVSALPIHQDWMGSEKFKCKVNNKDLPAPIERTI	358						
Qy	247	---PGQRPDPQVTVTLPPSRDELTKNQSLTCLVKGFVPSDIAVEWESNGQPENNYKTTTP	303						
Db	359	SRPKGSVRAPQVYVLPPEEEMTKQVTLTCMTDFMPEDIYVETWNTNGKTELNYKNTPE	418						
Qy	304	VLDSGSGFFLYSLTVDKSRWQOGNVEFSCVMHEALHNHYTKQSLSLSPGK	354						

Db 419 VLDSGSYFMYSKURVEKKNWVERNSYSCSVVHGLNHHHTTKSFSTPGK 469

RESULT 2

GHU

Ig gamma-1 chain C region - human
 C:Species: Homo sapiens (man)
 C>Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text_change 09-Jul-2004
 C:Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146
 R:Ellison, J.W.; Berson, B.J.; Hood, L.E.
 Nucleic Acids Res. 10, 4071-4079, 1982
 A>Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
 A:Reference number: A93433; MUID:82274238; PMID:6287432
 A:Accession: A93433
 A:Molecule type: DNA
 A:Residues: 1-330 <ELL>
 A:CROSS-references: UNIPROT:P01857; EMBL:Z17370
 A>Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers,
 A>Note: Lys-330 is removed after translation
 R:Harris, L.J.
 submitted to the EMBL Data Library, October 1992
 A:Reference number: S33904
 A:Accession: S36861
 A:Molecule type: DNA
 A:Residues: 2-330 <HAR>
 A:CROSS-references: EMBL:Z17370
 R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
 Cell 29, 671-679, 1982
 A>Title: Structure of human immunoglobulin gamma genes: implications for evolution of a
 A:Reference number: S33887; MUID:83001943; PMID:6811139
 A:Accession: S33887
 A:Molecule type: DNA
 A:Residues: 88-113/235-330 <TAK>
 A:CROSS-references: EMBL:Z17370
 R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gortlieb, P.D.; Waxdal, M.J.; Edelman,
 Biochemistry 9, 3161-3170, 1970
 A>Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen
 A:Reference number: A90563; MUID:71064024; PMID:5489771
 A:Contents: myeloma protein Eu
 A:Accession: B90563
 A:Molecule type: protein
 A:Residues: 1-96, 'R', 98-135 <CUN>
 A>Note: this sequence has the G1m(3) marker, 97-Arg
 R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
 Biochemistry 9, 3171-3181, 1970
 A>Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequen
 A:Reference number: A90564; MUID:71064025; PMID:5530842
 A:Contents: Eu
 A:Accession: A90564
 A:Molecule type: protein
 A:Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240,
 A>Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met
 R:Ponstingl, H.; Hilschmann, N.
 Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
 A>Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),
 igen Primaerstruktur.
 A:Reference number: A91668; MUID:77070269; PMID:826475
 A:Contents: myeloma protein Nie
 A:Accession: B91668
 A:Molecule type: protein
 A:Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27
 A>Note: this sequence has the G1m(17) and G1m(1) markers
 R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
 Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
 A>Title: Die Primaerstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KOI
 A:Reference number: A91723; MUID:83289131; PMID:6884994
 A:Contents: myeloma protein KOI; disulfide bonds
 A:Accession: A91723
 A:Molecule type: protein
 A:Residues: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH
 A>Note: this sequence has the G1m(3) and G1m(non-1) markers
 R:Gall, W.E.; Edelman, G.M.
 Biochemistry 9, 3188-3196, 1970

A>Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
 A:Reference number: A90565; MUID:71064027; PMID:4923144
 A:Contents: annotation; disulfide bonds
 R:Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
 Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
 A>Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
 enbromide cleavage products, and the disulfide bridges.
 A:Reference number: A91667; MUID:77070267; PMID:1002129
 A:Contents: annotation; disulfide bonds
 C:Genetics:
 A:Gene: GDB:IGHG1
 A:CROSS-references: GDB:120085; OMIM:147100
 A:Map position: 14q32.33-14q32.33
 C:Introns: 99/1; 114/1; 224/1
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
 bain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
 F:20-85/Domain: immunoglobulin homology <IM1>
 F:137-206/Domain: immunoglobulin homology <IM2>
 F:243-310/Domain: immunoglobulin homology <IM3>
 F:27-83,144-204,250-308/Disulfide bonds: #status experimental
 F:103/Disulfide bonds: interchain (to light chain) #status experimental
 F:109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
 F:180/Binding site: carbohydrate (Asn) (covalent) #status experimental
 Query Match 59.5%; Score 1116; DB 1; Length 330;
 Best Local Similarity 66.7%; Pred. No. 4.2e-60;
 Matches 220; Conservative 0; Mismatches 0; Indels 110; Gaps 1;
 Qy 135 ASTKGPSVFLAPSKSTSGTAAALGCLVKDYPEPVTVSNWNSGALTSGVHTFPVAVLQSS 194
 Db 1 ASTKGPSVFLAPSKSTSGTAAALGCLVKDYPEPVTVSNWNSGALTSGVHTFPVAVLQSS 60
 Qy 195 GLYSLSSVTVFPSSSLGTQYICNVNHPSTKVDKVEPKSCDKHTCTCPCP----- 247
 Db 61 GLYSLSSVTVFPSSSLGTQYICNVNHPSTKVDKVEPKSCDKHTCTCPCPAPPELLGG 120
 Qy 248 ----- 247
 Db 121 PSVFLFPKPKDITLMISTRPTVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
 Qy 248 -----GQPREPQVYTLPPSRDE 264
 Db 181 STYRWVSVLTVLHODWLNKEYCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRDE 240
 Qy 265 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFYLSTKLTVDKSRW 324
 Db 241 LTRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFYLSTKLTVDKSRW 300
 Qy 325 QQGNVFCVSWVMEALHNHYTQKSLSLSPGK 354
 Db 301 QQGNVFCVSWVMEALHNHYTQKSLSLSPGK 330
 RESULT 3
 S40295
 Ig gamma-2a chain (mAb735) - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
 C:Accession: S40295
 R:Kiebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; Bi
 submitted to the EMBL Data Library, January 1993
 A:Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 against
 A:Reference number: S40295
 A:Accession: S40295
 A:Molecule type: protein
 A:Residues: 1-446 <KLE>
 A:CROSS-references: UNIPROT:Q99L25
 C:Genetics:
 A:Map position: 12
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid


```

Db      241  ISTINPCPCKECHKCPAPNLEGGSPVFIFFPNIKDVLMLSLTPKVTCTVVVDVSDDDPDV 300
Qy      245  -----PCP-- 247
Db      301  QISFVNVVHTAQOTQTHREDYNSTIRVSTLPIQHODWMSGKEFKCKVNNKOLPSPIE 360
Qy      248  -----GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT 300
Db      361  RTISKIKGLVRAQVYILPPPAEQLSRKDVSLTCLVGVFNPGDISVETWSNGHTTEENYKD 420
Qy      301  TPPVLDSGSGFLYSKLTVDKSRWQGNVFCSGVMHEALHNNHYQKSLSPGK 354
Db      421  TAPVLDSGSGFYISKLNKMTSKMEKTDSCFSCNVRHEGLKNLYLKTTISRSPGK 474

RESULT 5
S01321
Ig gamma-2b chain precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999
C:Accession: S01321
R:de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.
Eur. J. Biochem. 176, 287-295, 1988
A>Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed a
A:Reference number: S01320; MUID:88329081; PMID:3138116
A:Accession: S01321
A:Molecule type: mRNA
A:Residues: 1-475 <DEL>
A:CROSS-references: EMBL:X13188; NID:g51780; PID:CAA31580.1; PID:g51781
A>Note: this sequence was determined from the differentiated gene
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-475/Product: Ig gamma-2b chain #status predicted <MAT>
F:159-233/Domain: immunoglobulin homology <IMM>

Query Match      54.9%; Score 1030.5; DB 2; Length 475;
Best Local Similarity 45.0%; Pred. No. 8.3e-55;
Matches 214; Conservative 47; Mismatches 99; Indels 123; Gaps 5;

Qy      1  MGWSLLFLVAVTRVLVSQVLQSGAEVVKPGASVKISCKASGYTFDTHAIHWKQNP 60
Db      1  MEWIFILFSLTAGVQSGVQLQSGAEVVKPGASVKISCKASGYTLTSGISWVKQRT 60
Qy      61  GQLEWIGYFSPGNDDFKYNRFKGAATLTADTASTAYVELSLRSRDTAVYFCTRS-- 118
Db      61  GQLEWIGEIFPGSGNSVFNEKFKGKATLTVDKSSSTAYLHLSLTSDESAVYFCAGPRQ 120
Qy      119  ---LNMAYWGQGLTVTVSSASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPPFVTVSW 175
Db      121  VGLLPFGYWGQGLTVTASAAKTPPSVYPLAPGCGDTTSGSVTLGCLVKGYFPESVTVTW 180
Qy      176  NSGALTSGVHTFPAVLQSSGLYSLSVVTVPSSSLGTQTYICNNVHKPSNTKVDKVEPK 235
Db      181  NSGSLSSVHTFPAVLQ--SGLYTWSSSVTVPSSTWPSQTVCVAHPASSTVTDKLEPS 239
Qy      236  S-----CDKTHTCP----- 244
Db      240  GPTSTINPCPCKECHKCPAPNLEGGSPVFIFFPNIKDVLMLSLTPKVTCTVVVDVSDDDP 299
Qy      245  -----PCP 247
Db      300  DVQISWVNVNVEVLTQAQTQTHREDYNSTIRVVSALPIQHODWMSGKEFKCKVNNKOLPAP 359
Qy      248  -----GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 298
Db      360  IERTISKIKGLVRAQVYILPPPAEQLSRKDVSLTCLVGVFNPGDISVETWSNGHTTEENY 419
Qy      299  KTTTPVLDSGSGFFLYSKLTVDKSRWQGNVFCSGVMHEALHNNHYQKSLSPGK 354
Db      420  KDTAPVLDSGSGFYISKLNKMTSKMEKTDSCFSCNVRHEGLKNLYLKTTISRSPGK 475

```

RESULT 6

G2HU

```

Ig gamma-2 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 09-Jul-2004
C:Accession: A93906; A92809; A90752; A93132; A02148
R:Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A>Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con
A:Reference number: A93906; MUID:82197621; PMID:6804948
A:Accession: A93906
A:Molecule type: DNA
A:Residues: 1-326 <ELL>
A:CROSS-references: UNIPROT:P01859; GB:V00554; GB:J00230; NID:g32759; PIDN:CA858438.1;
A>Note: Lys-326 is probably removed posttranslationally
R:Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A>Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f
A:Reference number: A92809; MUID:81007873; PMID:6774012
A:Contents: myeloma protein Til
A:Accession: A92809
A:Molecule type: protein
A:Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>
A>Note: Trp-156 is at or near the complement-binding site
R:Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A>Title: The amino acid sequences of the three heavy chain constant region domains of a
A:Reference number: A90752; MUID:80001357; PMID:113060
A:Contents: myeloma protein Zie
A:Accession: A90752
A:Molecule type: protein
A:Residues: 1-24, 'E', 26-57, 'EV', 60-85, 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-
A>Note: this sequence has since been revised
R:Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A>Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g
A:Reference number: A93132; MUID:80114419; PMID:118920
A:Contents: Zie
A:Accession: A93132
A:Molecule type: protein
A:Residues: 238-275 <HOP>
R:Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A:Reference number: A94591
A:Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A>Note: the revised sequence differs from that shown in having 60-Ala and in the amidati
ned
R:Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A>Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A:Reference number: A90253; MUID:72033500; PMID:4940472
A:Contents: annotation; myeloma protein Sa, disulfide bonds
R:Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A>Title: Structural studies of immunoglobulin G.
A:Reference number: A93157; MUID:69064124; PMID:5782707
A:Contents: annotation; Sa, disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG2
A:CROSS-references: GDB:119338; OMIM:147110
A:Map position: 14q32.33-14q32.33
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:133-202/Domain: immunoglobulin homology <IM1>
F:239-306/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: interchain (to light chain) #status experimental
F:27-83, 140-200, 246-304/Disulfide bonds: #status experimental
F:102, 103, 106, 109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

```

Query Match 53.6%; Score 1006; DB 1; Length 326;
 Best Local Similarity 61.1%; Pred. No. 1.6e-53;
 Matches 201; Conservative 7; Mismatches 9; Indels 112; Gaps 2;

QY 135 ASTKGSVPFLPASPXSSTSGTAAALCKLVKDYPEPEVTVVSNWNGALTSQVHTFPVQLSS 194
 DB 1 ASTKGSVPFLPASPXSSTSGTAAALCKLVKDYPEPEVTVVSNWNGALTSQVHTFPVQLSS 60
 QY 195 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKKVPKSCDKTHTCPPCP----- 247
 DB 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKTVVERKCCVE---CPPCPAPPVAGP 117
 QY 248 ----- 247
 DB 118 SVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNKTKPREEQFNS 177
 QY 248 -----GQPREPQVYTLPPSRDEL 265
 DB 178 TFRVSVLTVVHODWLNKEYKCKVSNKGLPAPIEKTIKTKGQPREPQVYTLPPSRDEM 237
 QY 266 TKNQVSLTCLVKGFPSPSDIAVESNGQPENNYKTTTPVLDSGFSFLYSKLTVDKSRWQ 325
 DB 238 TKNQVSLTCLVKGFPSPSDIAVESNGQPENNYKTTTPMLDSGFSFLYSKLTVDKSRWQ 297
 QY 326 QGNVFCSCVMEALHNHYTKLSLSLSPGK 354
 DB 298 QGNVFCSCVMEALHNHYTKLSLSLSPGK 326

RESULT 7
 A23511
 Ig gamma-3 chain C region (allotype G3m(b)) - human
 C;Species: Homo sapiens (man)
 C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
 C;Accession: A23511
 R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
 Nucleic Acids Res. 14, 1779-1789, 1986
 A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: cco
 A;Reference number: A23511; MUID:86148507; PMID:3081877
 A;Accession: A23511
 A;Molecule type: DNA
 A;Residues: 1-377 <HUC>
 A;Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
 C;Genetics:
 A;Gene: GDB:IGHG3
 A;Cross-references: GDB:119339; OMIM:147120
 A;Map position: 14q32.33-14q32.33
 A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
 C;Superfamily: immunoglobulin C region; immunoglobulin homology
 C;Keywords: immunoglobulin
 F;20-85/Domain: immunoglobulin homology <IMW>

Query Match 53.2%; Score 997.5; DB 2; Length 377;
 Best Local Similarity 53.8%; Pred. No. 6.2e-53;
 Matches 203; Conservative 8; Mismatches 9; Indels 157; Gaps 2;

QY 135 ASTKGSVPFLPASPXSSTSGTAAALCKLVKDYPEPEVTVVSNWNGALTSQVHTFPVQLSS 194
 DB 1 ASTKGSVPFLPASPXSSTSGTAAALCKLVKDYPEPEVTVVSNWNGALTSQVHTFPVQLSS 60
 QY 195 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKKV----- 232
 DB 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKRVLTKTPLGDTHTTCRCPKPKSC 120
 QY 233 -----BPKSCDKTHTCPPCP----- 247
 DB 121 DTTPPCPRCPKPKSCDTPPCPRCPKPKSCDTPPCPRCPAPPELLGGPSVFLFPPKPKDT 180
 QY 248 ----- 247
 DB 181 LMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNKTKPREEQYNSTFRVSVLTVLH 240

Qy	248	-----CQPREPQVYITLPPSRDELTKNOVSLTCLVK	277
		: : : : :	
Db	241	QDWLNGKEYKCKVSNKALPAPIEKTISKTKGQPREPQVYITLPPSRREENTKNOVSLTCLVK	300
Qy	278	GFVPSDIADVWESNGQPENNYKTTTPVLDSGSPFLYSKLTVDKSRWQGNVFPSCVMHE	337
		: : : : :	
Db	301	GFVPSDIADVWESNGQPENNTTPPMLDSGSPFLYSKLTVDKSRWQGNIFSCVMHE	360
Qy	338	ALHNHYTQKSLSLSPGK	354
		:	
Db	361	ALHNRFTQKSLSLSPGK	377
RESULT 8			
A60764			
Ig gamma-3 chain C region, form LAT - human			
C/Species: Homo sapiens (man)			
C/Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004			
C/Accession: A60764			
R/Huck, S.; Lefranc, G.; Lefranc, M.P.			
Immunogenetics 30, 250-257, 1989			
A/Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGH			
A/Reference number: A60764; MUID:90007613; PMID:2571587			
A/Accession: A60764			
A/Status: preliminary			
A/Molecule type: DNA			
A/Residues: 1-377 <HUC>			
A/Cross-references: UNIPROT:Q8N4Y9			
C/Superfamily: immunoglobulin C region; immunoglobulin homology			
C/Keywords: immunoglobulin			
F/20-85/Domain: immunoglobulin homology <IMM>			
Query Match	53.1%	Score 995.5; DB 2; Length 377;	
Best Local Similarity	53.8%;	Pred. No. 8.2e-53;	
Matches	203; Conservative	8; Mismatches	9; Indels 157; Gaps 2
Qy	135	ASTKGPSVFFLAPSKSTSGTGAALGCLVKDYFPEPVTVSNWNSGALTSGVHTFPAVLQSS	194
		: : : : :	
Db	1	ASTKGPSVFFLAPCSRSTSGTGAALGCLVKDYFPEPVTVSNWNSGALTSGVHTFPAVLQSS	60
Qy	195	GLYSLSVTVTPSSSLGTQYICNVNHKPSNTKVDKKV-----	232
		: : : : :	
Db	61	GLYSLSVTVTPSSSLGTQYTCNVNHKPSNTKVDKRVELKTPGLDTHTCPCPEPKSC	120
Qy	233	-----EPKSCDKHTCTCPCP-----	247
		:	
Db	121	DTPPPCPCPEPKSCDTPPCPCPEPKSCDTPPCPCPAPELLGGPSVFLFPPKPKDT	180
Qy	248	-----	247
Db	181	LMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKTKPREEQYNSTFRVSVLTVLH	240
Qy	248	-----CQPREPQVYITLPPSRDELTKNOVSLTCLVK	277
		: : : : :	
Db	241	QDWLNGKEYKCKVSNKALPAPIEKTISKTKGQPREPQVYITLPPSRREENTKNOVSLTCLVK	300
Qy	278	GFVPSDIADVWESNGQPENNYKTTTPVLDSGSPFLYSKLTVDKSRWQGNVFPSCVMHE	337
		: : : : :	
Db	301	GFVPSDIADVWESNGQPENNTTPPVLDSGSPFLYSRLTVDKSRWQGNVFPSCVMHE	360
Qy	338	ALHNHYTQKSLSLSPGK	354
		:	
Db	361	ALHNRFTQKSLSLSPGK	377
RESULT 9			
PC4436			
monoclonal antibody 13-1 heavy chain - mouse (fragment)			
C/Species: Mus musculus (house mouse)			
C/Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000			
C/Accession: PC4436			
R/Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.;			
Biochem. Biophys. Res. Commun. 240, 566-572, 1997			

A;Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyrin
A;Reference number: JCS810; MUID:98063277; PMID:9398605
A;Accession: PC4436
A;Molecule type: protein
A;Residues: 1-444 <AKA>
C;Comment: This catalytic antibody has peroxidase oxidase activity. It is directed against hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F:251-320/Domain: immunoglobulin homology <IMM>
F:22/Disulfide bonds: interchain (to 98) #status predicted
F:99/Disulfide bonds: interchain (to 109) #status predicted

Query Match 52.3%; Score 981.5; DB 2; Length 444;
Best Local Similarity 41.9%; Pred. No. 6.7e-52;
Matches 188; Conservative 66; Mismatches 76; Indels 119; Gaps 5;

QY 20 QVQLVQSGAEVVKPGASVKISKASGYTFTDTHAIHWKQNPQRLEWIGYSPGNDDF-- 77
Db 1 EQVQVETGGGLVPGNSKLSCLTSGFTFSRMHLWPPGKRLWIAVITKSDNYGA 60

QY 78 KYNERFKGKATLADTSASTAYVELSLRSEDYAVYFCR--LNMAVWGQGLTVTVSS 134
Db 61 KYAESVGRGFTISRDDSKSSVYLQWNLREEDTATYYCCRTIPWVYAMDCWGQTSVIYSS 120

QY 135 ASTKPSVFPPLAPSKSTSGTAAAGCLVKDYFPEPTVTVSNWNSGALTSGVHTFPAVLQSS 194
Db 121 AKTTPPSVYPLAPGSAAGTSMVTLGCLVKGYFPEPTVTVSNWNSGALTSGVHTFPAVLQSD 180

QY 195 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPPC----- 246
Db 181 -LYTLSSSVTVTPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPPC----- 246

QY 247 ----- 246
Db 236 SVFIFPPKPKDVLITITLTKVTVVVDISKDPEVQFQSFVDDVEVHTAQTQPREEQFNS 295

QY 247 -----PGPREPQVTLPPSRDEL 265
Db 296 TFRSVSELPIMHQDWLNGKEFKCRVNSAAPPAPAEIKTISKYGRKPAQVYTIPTPPKEQM 355

QY 266 TKNQVSLTCLVKGYFSPDSIAEVESWGQPNENYKTPPVLDSGDSFLLYSLKLTVDKSRWQ 325
Db 356 AKDKVSLTCMTIDFPEDITVEWQNGQPAENYKNTQFIMTDGDSFYFVSKLVNPKSNWE 415

QY 326 QGNVFCSCVMHEALHNHYTQKLSLSLSPGK 354
Db 416 AGNTFTCSVLNHEGLHNHYTQKLSLSLSPGK 444

RESULT 10
G4HU
I; gamma-4 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 02-Apr-1982 #sequence revision 02-Apr-1982 #text_change 09-Jul-2004
C;Accession: A90933; A90249; A02150
R;Ellison, J.; Buxbaum, J.; Hood, L.
A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A;Reference number: A90933; MUID:83157104; PMID:6299562
A;Accession: A90933
A;Molecule type: DNA
A;Residues: 1-327 <ELL>
A;Cross-references: UNIPROT:P01861
A;Note: The sequence was determined from the germline gene
R;Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A;Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant r
A;Reference number: A90249; MUID:70207560; PMID:4192699
A;Accession: A90249
A;Molecule type: protein
A;Residues: 1-30;81-326 <PIN>
C;Genetics:
A;Gene: GDB:IGHG4
A;Cross-references: GDB:119340; OMIM:147130

A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 111/1; 221/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:99-110/Region: hinge
F:134-203/Domain: immunoglobulin homology <IM2>
F:240-307/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: interchain (to light chain) #status experimental
F:27-83,141-201,247-305/Disulfide bonds: #status predicted
F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 51.9%; Score 974.5; DB 1; Length 327;
Best Local Similarity 59.7%; Pred. No. 1.3e-51;
Matches 197; Conservative 9; Mismatches 11; Indels 113; Gaps 2;

QY 135 ASTKPSVFPPLAPSKSTSGTAAAGCLVKDYFPEPTVTVSNWNSGALTSGVHTFPAVLQSS 194
Db 1 ASTKPSVFPPLAPSKSTSGTAAAGCLVKDYFPEPTVTVSNWNSGALTSGVHTFPAVLQSS 60

QY 195 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPPC----- 247
Db 61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKTHTCPPC----- 247

QY 248 ----- 247
Db 118 PSVFLFPPKPKDLMISRTPEVTCVVVDVSDPEVQFNWYVDGVFNHNAKTKPREEQFN 177

QY 248 -----GQPREPQVTLPPSRDE 264
Db 178 STYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVTLPPSQEE 237

QY 265 LTRNQVSLTCLVKGYFSPDSIAEVESWGQPNENYKTPPVLDSGDSFLLYSLKLTVDKSRW 324
Db 238 MTKNQVSLTCLVKGYFSPDSIAEVESWGQPNENYKTPPVLDSGDSFLLYSLKLTVDKSRW 297

QY 325 QGNVFCSCVMHEALHNHYTQKLSLSLSPGK 354
Db 298 QEGNVFCSCVMHEALHNHYTQKLSLSLSPGK 327

RESULT 11
S22080
I; heavy chain precursor (B/MT.4A.17.H5.A5) - bovine
N;Alternate names: Ig gamma-1 chain C region (clone 8.10)
C;Species: Bos primigenius taurus (cattle)
C;Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S22080; S06610; A31303
R;Sanders, P.G.
Submitted to the EMBL Data Library, November 1991
A;Reference number: S22080
A;Accession: S22080
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-470 <SAN>
A;Cross-references: EMBL:X62916; NID:9439; PIDN:CAA44699.1; PID:9440
R;Symons, D.B.A.; Clarkson, C.A.; Beale, D.
Mol. Immunol. 26, 841-850, 1989
A;Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gamma
A;Reference number: S06610; MUID:90097956; PMID:2513487
A;Accession: S06610
A;Molecule type: DNA
A;Residues: 142-470 <SYM>
A;Cross-references: EMBL:X16701
A;Note: the sequence was determined from the germline gene
C;Genetics:
A;Gene: Ig CH gamma-1
A;Introns: 98/1; 111/1; 221/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein

F:161-225/Domain: immunoglobulin homology <IMM>

F:318/Binding site: carbohydrate (Aen) (covalent) #status predicted

Query Match 50.4%; Score 946; DB 2; Length 470;

Best Local Similarity 42.2%; Pred. No. 9.7e-50;

Matches 201; Conservative 51; Mismatches 90; Indels 134; Gaps 10;

```
QY 3 WSLILLFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYFTDTHAIHWKQNPQG 62
DQ 5 WT--LLFVLSAPIGVLSQVQLVQSGAEVVKPGASVKISKASGYFTDTHAIHWKQNPQG 62
QY 63 RLEWIGYSPGNDPKYNERKFKATLTADTSASTAYVELSLRSEDYAVFYCTRSLNNA 122
DQ 63 ALEWVGITSGTIV--YNPALKSRSLITKENSQVLSVSVTPEDTATYCAR--T 118
QY 123 Y-----WGQGLTVTVSSASTKGPSVFPPLAPSSKSTGGTAAALGCLVKDYFPEPV 171
DQ 119 YGEVGDGAIDAWGGLLTVSSASTAPKVPYPLSSCCGDKSSSTVTLGLCLVSSYMPFV 178
QY 172 TVSNWNGALTSVHTFPVAVLQSSGLYSLSVTVVPSSTLGTQTYICNVNHPKSNTKVDKK 231
DQ 179 TVTNWNGALTSVHTFPVAVLQSSGLYSLSVTVVPSSTLGTQTYICNVNHPKSNTKVDKA 237
QY 232 VE-----PKCDKTHTCPP--CPGP----- 250
DQ 238 VDPTCKPSPCD---CCPPPELPGSPVFIFFPKPKDILTISGTPVTCVVDVGHDDPEV 294
QY 251 ----- 250
DQ 295 KFSFVDDVEVNTATTKPREOFNSTYRVVSALRIHQDWTGKKEFKCKVHNEGLPAPIV 354
QY 251 -----REPOVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVESNGOP--ENNY 298
DQ 355 RTISSTKGPAREPOVYVLAAPPQELSKSTLSVTCLMTVSYFDYIAVEWQNGQPESEDKY 414
QY 299 KTTTPVLSDGSEFFLYSKLTVDKSRWQGNVFCSCVMEALHNHYTKSLSPGK 354
DQ 415 GTTPQLDADSSYFLYSLRVDNRNSWQEGDYTCVMEALHNHYTKSLSPGK 470
```

RESULT 12

S31459

Ig gamma-1 chain - sheep (fragment)

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999

C:Accession: S31459

R:Patel, S.; Nau, P.

submitted to the EMBL Data Library, December 1992

A:Reference number: S31459

A:Accession: S31459

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-472 <PAT>

A:Cross-references: EMBL:X69797

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: immunoglobulin

F:277-346/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 50.1%; Score 940; DB 2; Length 472;

Matches 198; Conservative 56; Mismatches 95; Indels 124; Gaps 7;

```
QY 3 WSLILLFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYFTDTHAIHWKQNPQG 62
DQ 3 WT--LLFVLSAPIGVLSQVQLVQSGAEVVKPGASVKISKASGYFTDTHAIHWKQNPQG 60
QY 63 RLEWIGYSPGNDPKYNERKFKATLTADTSASTAYVELSLRSEDYAVFYCTR----- 117
DQ 61 ALEWIG--GSGYDEDIDYNPVLSKSLITKTSKQVSLTSTVTEDTAVYCARVDYS 119
QY 118 SLNWAY-----WGQGLTVTVSSASTKGPSVFPPLAPSSKSTGGTAAALGCLVKDYFPEPV 172
DQ 120 SHAFAYASYDFWGFGLLSLVLSASTTPPKVPLTSSCCGDTSSIVTLGCLVSSYMPFVPT 179
```

```
QY 173 VSNWNGALTSVHTFPVAVLQSSGLYSLSVTVVPSSTLGTQTYICNVNHPKSNTKVDKKY 232
DQ 180 VTWNSGALTSVHTFPVAVLQSSGLYSLSVTVVPSSTLGTQTYICNVNHPKSNTKVDKRV 239
QY 233 EPKSCDKTHTC-----PPCP----- 247
DQ 240 EPGCPDPCKHCRCPPELPGSPVFIFFPKPKDILTISGTPVTCVVDVGHDDPEVQPS 299
QY 248 ----- 247
DQ 300 WFDVNEVVRTARTKPREOFNSTYRVVSALRIHQDWTGKKEFKCKVHNEGLPAPIVRTI 359
QY 248 ---CQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVESNGOP--ENNYKTT 301
DQ 360 SRTKGQAREPOVYVLAAPPQELSKSTLSVTCLMTVSYFDYIAVEWQNGQPESEDKYGT 419
QY 302 PPVLSDGSEFFLYSKLTVDKSRWQGNVFCSCVMEALHNHYTKSLSPGK 354
DQ 420 TSQLDADSSYFLYSLRVDNRNSWQEGDYTCVMEALHNHYTKSLSPGK 472
```

RESULT 13

S69339

Ig heavy chain V region precursor - human

C:Species: Homo sapiens (man)

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000

C:Accession: S69339; S72664

R:Khamilichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.

Eur. J. Biochem. 229, 54-60, 1995

A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.

A:Reference number: S69339; MUID:95262687; PMID:7744049

A:Accession: S69339

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-374 <KGA>

A:Cross-references: EMBL:X81695

R:Khamilichi, A.A.

submitted to the EMBL Data Library, September 1994

A:Reference number: S72664

A:Accession: S72664

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-140,'C',142-374 <KH2>

A:Cross-references: EMBL:X81695

C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 45.4%; Score 852; DB 2; Length 374;

Best Local Similarity 48.8%; Pred. No. 3.3e-44;

Matches 185; Conservative 44; Mismatches 106; Indels 44; Gaps 9;

```
QY 8 LFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYFTDTH--AIHWKQNPQORLE 65
DQ 8 LLLLTIPSWSLVSQITLKESGFTLVKPTQTTLTCTFGSFLSKSGVGWIRPQGOALE 67
QY 66 WIGYSPGNDPKYNERKFKATLTADTSASTAYVELSLRSEDYAVFYCTRSL---NWA 122
DQ 68 WLALIF--WDDDKRYSPSLRTRLTITKDTSKNQVLTMTNVDPADTATYCYSGVSGYGG 126
QY 123 Y---WGQGLTVTVSSASTK-----GPSVFPLAPSSKST--SGGTAAL 159
DQ 127 YRFHSWGQGLTVTVSSSEPKSCDKTHCTCPAPPELLGGPSVFLPPKPKDTLMISRTPEV 186
QY 160 GCLVKDYFPEPVTVSWN---SGALTSGVHTFPAVLQSSGLYSLSVTVVPSST--LGTQTY 215
DQ 187 TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY 246
QY 216 ICNVNHPKSNTKVDKVEPKSCDKTHCTCPGCPGPREPOVYTLPPSRDELTKNQVSLTCL 275
DQ 247 KCVISNKAALPAPIEK-----TISKAKGPREPOVYTLPPSRDELTKNQVSLTCL 295
QY 276 VKGYFVPSDIAVESNGOPENNYKTTTPVLSDGSEFFLYSKLTVDKSRWQGNVFCSCV 335
```

```
Db 296 VKGYFVPSDIATWESNGQPNYKTTTPVLDSDGSEFFLYSKLTVDKSRWQGNVPSCSVM 355
Qy 336 HEALHNHYTKQSLSPGK 354
Db 356 HEALHNHYTKQSLSPGK 374

RESULT 14
S69131
Ig heavy chain (DOT) - human (fragment)
N:Alternate names: anti-riboflavin Igg Fd fragment
C:Species: Homo sapiens (man)
C:Date: 12-Feb-1998 #sequence_revision 22-May-1998 #text_change 21-Jan-2000
C:Accession: S69131
R:Stoppini, M.; Bellotti, V.; Negri, A.; Merlini, G.; Garver, F.; Ferri, G.
Eur. J. Biochem. 228, 886-893, 1995
A:Title: Characterization of the two unique human anti-flavin monoclonal immunoglobulins
A:Reference number: S69130; MUID:95255298; PMID:7737190
A:Accession: S69131
A:Molecule type: protein
A:Residues: 1-241 <STO>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: blocked amino end; heterotetramer; immunoglobulin; pyroglutamic acid
F:1-241/Product: Ig heavy chain (DOT) (fragment) #status experimental <WAT>
F:140-205/Domain: immunoglobulin homology <IMM>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 43.4%; Score 814.5; DB 2; Length 241;
Best Local Similarity 66.8%; Pred. No. 3.7e-42;
Matches 163; Conservative 23; Mismatches 47; Indels 11; Gaps 4;

Qy 20 QVQLVQSGAEVVKPGASVKISKASGYTFTDHAHVKQKQPGQRLWIGYFSPGNDDPKY 79
Db 1 QVQLVQSGAEVVKPGASVKISKASGYTFTDYYIHVKQKQPGEGLEWIGYFPGSGNTKY 60

Qy 80 NERFKGKATLTADTSASTAYVELSLRSEDNAVYFCTR---SLNWAYGQGTLPVAVLQSSGLY 197
Db 61 NEKFKGKATLTVDTSSTAYMQLSSLTSEDSAVYFCARGGKFAMDYWGQGTSTVTVSSAKT 120

Qy 138 KGPSVFPPLAPSSKSTSGTAAALGCLVKDYPEPPTVSWNSGALTSGVHTFPAVLQSSGLY 197
Db 121 TAPSVYPLAPVCGDTTSSVTLGCLVKGYPEPPTVLTWNSGSLSSGVHTFPAVLQSSD-LY 179

Qy 198 SLSSVVTVPSSSLGTQTYICNVNHPKNTKVDKKVEPKSCDKTHTCPPC-----PQQRPEP 253
Db 180 TLSSSVVTVPSSSTWPSQSTTCNVNHPASSTKVDKKIEPRG-PTIKPCPCPKCPAPNLLGGP 238

Qy 254 QVYTLPP 260
Db 239 SVFIIPP 245

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Db 296 VKGYFVPSDIATWESNGQPNYKTTTPVLDSDGSEFFLYSKLTVDKSRWQGNVPSCSVM 355
Qy 336 HEALHNHYTKQSLSPGK 354
Db 356 HEALHNHYTKQSLSPGK 374

RESULT 15
S38950
Ig gamma chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
C:Accession: S38950
R:Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; Biol. Chem. Hoppe-Seyler 374, 993-1000, 1993
A:Title: Primary structure of the murine monoclonal IgG2a antibody mAb735 against alpha
A:Reference number: S38950; MUID:94128242; PMID:8297501
A:Accession: S38950
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-246 <KLE>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:137-201/Domain: immunoglobulin homology <IMM>

Query Match 43.1%; Score 809; DB 2; Length 246;
Best Local Similarity 64.4%; Pred. No. 8.1e-42;
Matches 159; Conservative 28; Mismatches 52; Indels 8; Gaps 4;
```

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OM protein - protein search, using sw model

Run on: March 23, 2005, 18:05:41 ; Search time 136.475 Seconds
(without alignment)
1328.275 Million cell updates/sec

Title: US-10-058-069-7
Perfect score: 1876
Sequence: 1 MGRSLILLFLVAVATRVLSQ.....MHEALHNHYTKSLSLSPGK 354

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1521.5	81.1	469	Q7Z7P5	Q7Z7P5 homo sapien
2	1500.5	80.0	475	Q6N095	Q6N095 homo sapien
3	1479	78.8	480	Q6PJF1	Q6PJF1 homo sapien
4	1440	76.8	472	Q6N089	Q6N089 homo sapien
5	1439	76.7	518	Q6N030	Q6N030 homo sapien
6	1430.5	76.3	475	Q6MZQ6	Q6MZQ6 homo sapien
7	1427.5	76.1	544	Q6PJ95	Q6PJ95 homo sapien
8	1426	76.0	466	Q6IN78	Q6IN78 homo sapien
9	1425	76.0	470	Q6PJ44	Q6PJ44 homo sapien
10	1422.5	75.8	475	Q6GMW7	Q6GMW7 homo sapien
11	1417	75.5	466	Q6N096	Q6N096 homo sapien
12	1410	75.2	478	Q6PI81	Q6PI81 homo sapien
13	1407.5	75.0	473	Q6MZV7	Q6MZV7 homo sapien
14	1402	74.7	480	Q6N094	Q6N094 homo sapien
15	1400	74.6	482	Q7Z351	Q7Z351 homo sapien
16	1398.5	74.5	473	Q6P055	Q6P055 homo sapien
17	1392	74.2	470	Q7Z5W1	Q7Z5W1 homo sapien
18	1379.5	73.5	465	Q6GMX6	Q6GMX6 homo sapien
19	1377.5	73.4	481	Q6N097	Q6N097 homo sapien
20	1374	73.2	476	Q6GMX1	Q6GMX1 homo sapien
21	1330	70.9	464	Q6MZU6	Q6MZU6 homo sapien
22	1322	70.5	493	Q68CN4	Q68CN4 homo sapien
23	1285.5	68.5	465	Q6P6C4	Q6P6C4 homo sapien
24	1284.5	68.5	521	Q8N4Y9	Q8N4Y9 homo sapien
25	1218	64.9	417	Q6N093	Q6N093 homo sapien
26	1205	64.2	473	Q8TC63	Q8TC63 homo sapien
27	1195.5	63.7	476	Q6GMZ7	Q6GMZ7 homo sapien
28	1162	61.9	348	Q6PYX1	Q6PYX1 homo sapien
29	1148.5	61.2	465	Q6PJB2	Q6PJB2 mus musculus
30	1138.5	60.7	473	Q9D8L4	Q9D8L4 mus musculus
31	1121.5	59.8	463	Q99LC4	Q99LC4 mus musculus

32	1116	59.5	330	1	GC1_HUMAN	P01857 homo sapien
33	1101	58.7	470	2	Q7TKK1	Q7TKK1 mus musculus
34	1100	58.6	464	2	Q6PF95	Q6PF95 mus musculus
35	1096	58.4	472	2	Q6PJA7	Q6PJA7 mus musculus
36	1087.5	58.0	487	2	Q65ZL2	Q65ZL2 mus sp. fv/
37	1023	54.5	474	2	Q8R3H6	Q8R3H6 mus musculus
38	1006	53.6	326	1	GC2_HUMAN	P01859 homo sapien
39	987.5	52.6	509	2	Q8NE17	Q8NE17 homo sapien
40	986	52.6	458	2	Q65ZQ1	Q65ZQ1 homo sapien
41	974.5	51.9	327	1	GC4_HUMAN	P01861 homo sapien
42	974.5	51.9	473	2	Q91Z05	Q91Z05 mus musculus
43	959	51.1	464	2	Q6PIP8	Q6PIP8 mus musculus
44	924.5	49.3	471	2	Q66K04	Q66K04 mus musculus
45	891.5	47.5	354	2	Q86TT2	Q86TT2 homo sapien

ALIGNMENTS

RESULT 1
Q7Z7P5 PRELIMINARY; PRT; 469 AA.
AC Q7Z7P5
DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE IGHG1 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Splice;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzyszewski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Splice;
RA Strausberg R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC051328; AAHS1328.1; -;
DR HSSP; P01857; 1HZH;
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN 2.
SQ SEQUENCE 469 AA; 51395 MW; C8D5BE12BAAAF795C CRC64;

Query Match 81.1%; Score 1521.5; DB 2; Length 469;

RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Strausberg R.;
 RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC016381; AAH16381.1; -;
 DR HSSP; P01861; IADQ.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG-cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; CI-set; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGcl; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 480 AA; 52586 MW; 64DC641AE47CD6C8 CRC64;

Query Match 78.8%; Score 1479; DB 2; Length 480;
 Best Local Similarity 61.7%; Pred. No. 1.9e-97;
 Matches 296; Conservative 18; Mismatches 40; Indels 126; Gaps 2;
 QY 1 MGWLSILLFLVAVATRVLSQVQVVGAEVVKPGASVKISKASGYTFTDHAHHVKNP 60
 DB 1 MDWTRFLVVAATGVQVQVVGAEVVKPGASVKISKASGGSGFVSWVRQAP 60
 QY 61 QORLEWIGYFSGNDDFKYNRFKATLTADTSASTAYVELSLRSSEDTAVYFCTSL- 119
 DB 61 GQGLAWMGIIIPAFDITKYAQNFQDRVTISADESDTAYMELSLRSSEDTATYYCARDLA 120
 QY 120 -----NMAYWGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLV 164
 DB 121 LYELWSGPHTEKYYGLDVGWGGTPTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLV 180
 QY 165 DYFPEPTVTVSSNGALTSGVHTFPAVLQSSGLYSLSVTVTVSSSLGQTQYICNVNHRKPS 224
 DB 181 DYFPEPTVTVSSNGALTSGVHTFPAVLQSSGLYSLSVTVTVSSSLGQTQYICNVNHRKPS 240
 QY 225 NTKVDKKEPKSCDKTHTCPPCP----- 247
 DB 241 NTKVDKKEPKSCDKTHTCPPCPAPPELLGPGSVFLFPKPKDTLMSRTPEVTCVVVDVS 300
 QY 248 ----- 247
 DB 301 HEDPEVKFNWYDGVGVHNAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKA 360
 QY 248 -----GPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQP 294
 DB 361 LPAPLEKTIISKAGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQP 420
 QY 295 ENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 354
 DB 421 ENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 480

RESULT 4
 Q6N089
 ID Q6N089 PRELIMINARY; PRT; 472 AA.
 AC Q6N089;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Hypothetical protein DKFZp686p15220.
 GN Name=DKFZp686p15220;
 OS Homo sapiens (Human);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Human rectum tumor;

RG The German Human cDNA Consortium;
 RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
 RA Fobo G., Han M., Wiemann S.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX640627; CAE45781.1; -;
 DR HSSP; P01861; IADQ.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG-cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; CI-set; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGcl; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 76.8%; Score 1440; DB 2; Length 472;
 Best Local Similarity 59.3%; Pred. No. 1.1e-94;
 Matches 280; Conservative 33; Mismatches 41; Indels 118; Gaps 2;
 QY 1 MGWLSILLFLVAVATRVLSQVQVVGAEVVKPGASVKISKASGYTFTDHAHHVKNP 60
 DB 1 MELGTWIFLVAIILKGVQCEVQLVESGGGLVQPGKSLRSCAASGFTFDDYAMHWVRQAP 60
 QY 61 QORLEWIGYFSGNDDFKYNRFKATLTADTSASTAYVELSLRSSEDTAVYFCTSL- 119
 DB 61 GKGLWVSGISWNSGSIAYADSVKGRFTISRDNKNSLYLQWNSLRAREDYLYCAKEIG 120
 QY 120 -----NMAYWGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLV 172
 DB 121 AHNFYTYGMDVWGGTPTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLV 180
 QY 173 VSWNSGALTSGVHTFPAVLQSSGLYSLSVTVTVSSSLGQTQYICNVNHRKPSNTKVDKV 232
 DB 181 VSWNSGALTSGVHTFPAVLQSSGLYSLSVTVTVSSSLGQTQYICNVNHRKPSNTKVDKV 240
 QY 233 EPKSCDKTHTCPPCP----- 247
 DB 241 EPKSCDKTHTCPPCPAPPELLGPGSVFLFPKPKDTLMSRTPEVTCVVVDVSHEDPEVKF 300
 QY 248 ----- 247
 DB 301 NWYVDGVGVHNAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 360
 QY 248 -----GPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQENNYKTTTP 302
 DB 361 ISKAGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQENNYKTTTP 420
 QY 303 PVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 354
 DB 421 PVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 472

RESULT 5
 Q6N030
 ID Q6N030 PRELIMINARY; PRT; 518 AA.
 AC Q6N030;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Hypothetical protein DKFZp686p115212.
 GN Name=DKFZp686p115212;
 OS Homo sapiens (Human);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Human rectum tumor;

RG The German Human cDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.,
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; BX640724; CAE45841.1; -
DR HSSP; P01861; IADQ.
DR InterPro; IPR000005; HTHArac.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 518 AA; 57019 MW; 93B5F98613BF6382 CRC64;

Query Match 76.7%; Score 1439; DB 2; Length 518;
Best Local Similarity 55.6%; Pred. No. 1.5e-94;
Matches 288; Conservative 28; Mismatches 38; Indels 164; Gaps 3;

Qy 1 MGSLILLFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDHAHVKQNP 60
Db 1 MDWTWRLFLVTAAGTAHSAQVHLVQSGAEVVKPGASVKISCTAGSYFTFTFHNWVQAP 60

Qy 61 GQRLWIGYFPGNDDFKYNRPKATLTADTSASTAYVELSLRSEDATVVFCTSLN 120
Db 61 GQSLWGWINTGNKTKYKQFGQVITRTDWTITAYMDLSLRSEDATVAVWCARDAP 120

Qy 121 MA-----YQGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYPPVTV 173
Db 121 QGVTTTTFDYWGQGLTVTVSSASTKGPSVFPPLAPCSRSTSGTAAALGCLVKDYPPVTV 180

Qy 174 SWNSGALTSVHTTTPAVLQSSGLYSLSVTVTPSSSLGTQYICNVNHPKNTKVDKKV- 232
Db 181 SWNSGALTSVHTTTPAVLQSSGLYSLSVTVTPSSSLGTQYICNVNHPKNTKVDKRV 240

Qy 233 -----EPKSCDKTHTCPPC 246
Db 241 LKTPGLDTHTCPCPCPCDTPPCPCPCPCDTPPCPCPCPCDTPPCPCPC 300

Qy 247 P----- 247
Db 301 PAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNAKT 360

Qy 248 -----GQPREPOVY 256
Db 361 KPREEQYNSTRYVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKTGQPREPOVY 420

Qy 257 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 316
Db 421 TLPPSRDEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 480

Qy 317 LTVDKSRWQOQGNVFCSCVMHEALHNYHTQKSLSPGK 354
Db 481 LTVDKSRWQOQGNVFCSCVMHEALHNYHTQKSLSPGK 518

RESULT 6
Q6MZQ6 PRELIMINARY; PRT; 475 AA.
ID Q6MZQ6
AC Q6MZQ6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp6866g11190.
GN Name=DKFZp6866g11190;
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RG The German Human cDNA Consortium;
RA Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA Han M., Wiemann S.,
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; BX640947; CAE45972.1; -
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 52043 MW; B7EAE255A26F4B8E CRC64;

Query Match 76.3%; Score 1430.5; DB 2; Length 475;
Best Local Similarity 59.2%; Pred. No. 5.3e-94;
Matches 281; Conservative 36; Mismatches 37; Indels 121; Gaps 3;

Qy 1 MGSLILLFLVAVATRVLSQVQLVQSGAEVVKPGASVKISKASGYTFTDHAHVKQNP 60
Db 1 MEFLGLWFLVAILKGVQCEVQLLESGGLVQPGSLRLSCAASGFTFRYAMNVRQAP 60

Qy 61 GQRLWIGYFPGNDDFKYNRPKATLTADTSASTAYVELSLRSEDATVVFCTSLN 118
Db 61 GKLEWYSGISGSGVNTYADSVKGRFTISGDISINTLYLQMHSLRADDATVAVYCARADY 120

Qy 119 -----LNMA-----WGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPE 169
Db 121 RDQVSPAYVYFDVWGRGTLVSVSAASTKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPE 180

Qy 170 PVTVMNSGALTSGVHTTTPAVLQSSGLYSLSVTVTPSSSLGTQYICNVNHPKNTKVD 229
Db 181 PVTVMNSGALTSGVHTTTPAVLQSSGLYSLSVTVTPSSSLGTQYICNVNHPKNTKVD 240

Qy 230 KKVPEKSCDKTHTCPPC----- 247
Db 241 KKVPEKSCDKTHTCPPCPAPELIGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPE 300

Qy 248 ----- 247
Db 301 VKFNWYDGVGVHNAKTKPREQYNSTRYVSVLTVLHQDWLNGKEYKCKVSNKALPAPI 360

Qy 248 -----GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK 299
Db 361 EKTISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK 420

Qy 300 TTPPVLDSDGSFFLYSKLTVDKSRWQOQGNVFCSCVMHEALHNYHTQKSLSPGK 354
Db 421 TTPPVLDSDGSFFLYSKLTVDKSRWQOQGNVFCSCVMHEALHNYHTQKSLSPGK 475

RESULT 7
Q6PJ95 PRELIMINARY; PRT; 544 AA.
ID Q6PJ95
AC Q6PJ95;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_TaxID=9606;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Primary B-Cells;	
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;	
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,	
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,	
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,	
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,	
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	
RA	Fahy J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,	
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,	
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,	
RA	Jones S.J., Marra M.A.;	
RT	"Generation and initial analysis of more than 15,000 full-length human	
RT	and mouse cDNA sequences."	
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Primary B-Cells;	
RA	Strausberg R.;	
RL	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; BC019046; AAH19046.1; -	
DR	HSP; P01861; IADQ.	
DR	InterPro; IPR003599; Ig.	
DR	InterPro; IPR007110; Ig-like.	
DR	InterPro; IPR003597; Ig cl.	
DR	InterPro; IPR003006; Ig MHC.	
DR	InterPro; IPR003596; Ig v.	
DR	Pfam; PF07654; CI-set; 3.	
DR	SMART; SM00409; IG; 2.	
DR	SMART; SM00407; IG; 3.	
DR	SMART; SM00406; IG; 1.	
DR	PROSITE; PS00835; IG LIKE; 4.	
DR	PROSITE; PS00290; IG MHC; UNKNOWN_2.	
KW	Hypothetical protein.	
SQ	SEQUENCE 544 AA; 60102 MW; 1895814B2297C668 CRC64;	
Query Match 76.1%; Score 1427.5; DB 2; Length 544;		
Best Local Similarity 59.6%; Pred. No. 1e-93;		
Matches 282; Conservative 28; Mismatches 42; Indels 121; Gaps 2;		
Qy	1 MGWSLILFLVAVATRVLSQVLQVSGVAVKPGASVKISCKASGYTFTDHAHVKQNP 60	
Db	1 MEFGSLVFLVALLRGVQQAQLVSGGVQVPGSLRLSCLSAAGSFRPSYGMHVRQAP 60	
Qy	61 GQRLWICGFSPGNDFFKYNRFKQKATLTADTSASTAYVELLSLRSEDYVYFCTRS-- 118	
Db	61 GKGLWVAVFSDYEDSKTYAASVGRFTISRDNSKNTLSQVNSLRVEDYVYCAKQK 120	
Qy	119 -----LNMYVGQGTTLTVSSASTKGPSVFPPLAPSSKTSKGTAAALGLVKDYFPE 169	
Db	121 PWYSNSWFLTFDWSGRGTLTVSSASTKGPSVFPPLAPSSKTSKGTAAALGLVKDYFPE 180	
Qy	170 PVTWSNNGALTSVGHVTPAVLQSSGLYSLSVWTVPPSSSLGTQYICNVNHKPSNTKVD 229	
Db	181 PVTWSNNGALTSVGHVTPAVLQSSGLYSLSVWTVPPSSSLGTQYICNVNHKPSNTKVD 240	
Qy	230 KKVEPKSCDKTHCTCPCP----- 247	
Db	241 KKVEPKSCDKTHCTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE 300	
Qy	248 ----- 247	
Db	301 VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI 360	
Qy	248 -----GQREPOVYTLPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYK 299	
Db	361 EKTISKAKGQPREPOVYTLPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYK 420	
Qy	300 TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSP 352	
Db	421 TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSP 473	
RESULT 8		
QIDN78	PRELIMINARY; PRT; 466 AA.	
AC	Q6IN78; 05-JUL-2004 (TrEMBLrel. 27, Created)	
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)	
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)	
DE	IGH1 protein.	
GN	Name=IGH1;	
OS	Homo sapiens (Human)	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_TaxID=9606;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Peripheral Nervous System;	
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;	
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,	
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,	
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,	
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,	
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	
RA	Fahy J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,	
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,	
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,	
RA	Jones S.J., Marra M.A.;	
RT	"Generation and initial analysis of more than 15,000 full-length human	
RT	and mouse cDNA sequences."	
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Peripheral Nervous System;	
RA	Strausberg R.;	
RL	Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; BC072419; AAH72419.1; -	
DR	HSP; P01861; IADQ.	
DR	InterPro; IPR003599; Ig.	
DR	InterPro; IPR007110; Ig-like.	
DR	InterPro; IPR003597; Ig cl.	
DR	InterPro; IPR003006; Ig MHC.	
DR	InterPro; IPR003596; Ig v.	
DR	Pfam; PF07654; CI-set; 3.	
DR	SMART; SM00409; IG; 2.	
DR	SMART; SM00407; IG; 3.	
DR	SMART; SM00406; IG; 1.	
DR	PROSITE; PS00835; IG LIKE; 4.	
DR	PROSITE; PS00290; IG MHC; UNKNOWN_2.	
SQ	SEQUENCE 466 AA; 50853 MW; 53EB0BCDE81076E CRC64;	
Query Match 76.0%; Score 1426; DB 2; Length 466;		
Best Local Similarity 60.4%; Pred. No. 1.1e-93;		
Matches 282; Conservative 30; Mismatches 41; Indels 114; Gaps 3;		
Qy	1 MGWSLILFLVAVATRVLSQVLQVSGVAVKPGASVKISCKASGYTFTDHAHVKQNP 60	

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Db 1 MEFWLSVFLVAILKGVQCEVQLVBSGGGLIQPGGSLTSCAASGLTVSSNMHWROAP 60
Qy 61 GORLEWIGYFSGNDGDFKYNRFKQKATLTADTASTAYVELSLRSDEDTAVYFCTRS-- 118
Db 61 GKGLEWVSVLYIGGATY-YADSVKGRFTISRDNKNTLYLQWNSLRABEDTAVYVCARGNY 119
Qy 119 -LNMAVYQGGLTVTVSSASTKGPSVFPPLAPSKSTSGGTAALGCLVLDYFPEPVTVSNWS 177
Db 120 VVPAAPWGQGLTVTVSSASTKGPSVFPPLAPSKSTSGGTAALGCLVLDYFPEPVTVSNWS 179
Qy 178 GALTSGVHTFPVAVLQSSGLYSLSSVTVVPSSSLGTQTVICNVNKHPSNTKVDKVPKSC 237
Db 180 GALTSGVHTFPVAVLQSSGLYSLSSVTVVPSSSLGTQTVICNVNKHPSNTKVDKVPKSC 239
Qy 238 DKTHTCPPCP----- 247
Db 240 DKTHTCPPCPAPPELLGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVD 299
Qy 248 ----- 247
Db 300 GVEVHNAKTPREEQYNSTYRVVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTISKAK 359
Qy 248 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGYFSPDIAVEVESNGQPENNYKTTPPVLD 307
Db 360 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGYFSPDIAVEVESNGQPENNYKTTPPVLD 419
Qy 308 DGSFPLYSLKLTVDKSRWQGNVFCVSNVHEALHNHYTKSLSPGK 354
Db 420 DGSFPLYSLKLTVDKSRWQGNVFCVSNVHEALHNHYTKSLSPGK 466

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RESULT 9

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Q6PJ44
ID Q6PJ44 PRELIMINARY; PRT; 470 AA.
AC Q6PJ44;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavini T.L., Scheetz T.B.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Huxley
RA Faney J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

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DR EMBL; BC018747; AAH18747.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN 2.
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 51715 MW; 7B49556A11FD7D99 CRC64;

Query Match 76.0%; Score 1425; DB 2; Length 470;
Best Local Similarity 59.6%; Pred. No. 1.3e-93;
Matches 280; Conservative 31; Mismatches 43; Indels 116; Gaps 2;

Qy 1 MGWSLILLLFVAVATRVLSQVQLVQSGAEVVKPGASVKISCKASGYTFTDHAHMKQNP 60
Db 1 MELGLSWFLVAILLEGVQCEVQLVBSGGGLVQPGGSLRSCVSGFTFSSVWMSWROAP 60
Qy 61 GORLEWIGYFSGNDGDFKYNRFKQKATLTADTASTAYVELSLRSDEDTAVYFCTRSLN 120
Db 61 GKGLEWVANIKQDGSERKYYVDSVKGRFTISRDNKNSLYLQWNSLRABEDTAVYVCARDGS 120
Qy 121 MAY-----WGQTLTVTVSSASTKGPSVFPPLAPSKSTSGGTAALGCLVLDYFPEPVTVS 174
Db 121 SWYRDWFDPMGQGLTVTVSSASTKGPSVFPPLAPSKSTSGGTAALGCLVLDYFPEPVTVS 180
Qy 175 WNSGALTSGVHTFPVAVLQSSGLYSLSSVTVVPSSSLGTQTVICNVNKHPSNTKVDKVKVP 234
Db 181 WNSGALTSGVHTFPVAVLQSSGLYSLSSVTVVPSSSLGTQTVICNVNKHPSNTKVDKVKVP 240
Qy 235 KSCDKHTCTCPCP----- 247
Db 241 KSCDKHTCTCPCPAPPELLGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
Qy 248 ----- 247
Db 301 YVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTIS 360
Qy 248 ---GQPREPQVYTLPPSRDELTKNQVSLTCLVKGYFSPDIAVEVESNGQPENNYKTTPPV 304
Db 361 KAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGYFSPDIAVEVESNGQPENNYKTTPPV 420
Qy 305 LDSGSPFLYSLKLTVDKSRWQGNVFCVSNVHEALHNHYTKSLSPGK 354
Db 421 LDSGSPFLYSLKLTVDKSRWQGNVFCVSNVHEALHNHYTKSLSPGK 470

RESULT 10
Q6GMW7
ID Q6GMW7 PRELIMINARY; PRT; 475 AA.
AC Q6GMW7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

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```
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Faney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073782; AAH73782.1; -
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig.v.
DR Pfam; PF07654; Cl-set; 3.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 51987 MW; 2A1PES5D736860F8 CRC64;

Query Match 75.8%; Score 1422.5; DB 2; Length 475;
Best Local Similarity 59.6%; Pred. No. 2e-93;
Matches 283; Conservative 28; Mismatches 43; Indels 121; Gaps 3;

Qy 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISCKASGYTFTDHAIIHWKQP 60
Db 1 MEFGLSCVFLVAILKFGVHCVEQLVQSGGLVQPGSLKLSKCAASGFTVNNMHRVROAP 60

Qy 61 GORLEWIGYFSPGNDPFKYNRFKQKATLTADTASATAYVELSLRSDDTAVYFCTRS - 118
Db 61 GKGLVWVSLMRDDASETAYAEFFVQGRFTISRDNAKNTLFLQLSLRAEDTAVYICARGGF 120

Qy 119 LNMAWYGGTLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVMSNG 169
Db 121 RGDTCNLFYGLDVMGQGTTVIVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPE 180

Qy 170 PVTWSNAGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNITKVD 229
Db 181 PVTWSNAGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNITKVD 240

Qy 230 KKVEPKSCDKTHCTCPCP- - - - - 247
Db 241 KKVEPKSCDKTHCTCPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPE 300

Qy 248 - - - - - 247
Db 301 VKFNWYDGVGVHNAKTPREEQYNSTYRVVSVLTVLHQDLNMGKEYKCKVSNKALPAPI 360

Qy 248 - - - - - GQRPQVYTLPPSRDELTKNQVSLTCLVKGYFDPDSIAEWESNGQPENNYK 299
Db 361 EKTISKAKGQRPQVYTLPPSRDELTKNQVSLTCLVKGYFDPDSIAEWESNGQPENNYK 420

Qy 300 TTPPVLDSDGFFLYSKLTVDKSRWQQGNVFCSSVMHEALHNHYTOKLSLSLSPGK 354
Db 421 TTPPVLDSDGFFLYSKLTVDKSRWQQGNVFCSSVMHEALHNHYTOKLSLSLSPGK 475
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RESULT 11
Q6N096 PRELIMINARY; PRT; 466 AA.
AC Q6N096;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKF2p686115196.
GN Name=DKF2p686115196;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RG The German Human cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640620; CAB45774.1; -
DR HSSP; P01861; 1ADO.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig.v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 466 AA; 50926 MW; 01E91B748D6D57C4 CRC64;

Query Match 75.5%; Score 1417; DB 2; Length 466;
Best Local Similarity 60.3%; Pred. No. 4.8e-93;
Matches 281; Conservative 28; Mismatches 45; Indels 112; Gaps 2;

Qy 1 MGWSLILFLVAVATRVLSQVQLVQSGAEVVKPGASVKISCKASGYTFTDHAIIHWKQP 60
Db 1 MEFGLSCVFLVAILKFGVHCVEQLVQSGGLVQPGSLKLSKCAASGFTVNNMHRVROAP 60

Qy 61 GORLEWIGYFSPGNDPFKYNRFKQKATLTADTASATAYVELSLRSDDTAVYFCTRS - 118
Db 61 GKGLVWVSLMRDDASETAYAEFFVQGRFTISRDNAKNTLFLQLSLRAEDTAVYICARGGF 120

Qy 119 LNMAWYGGTLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVMSNG 178
Db 121 GNPDWGGQTLVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVMSNG 180

Qy 179 ALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNITKVDKVEPKSCD 238
Db 181 ALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNITKVDKVEPKSCD 240

Qy 239 KTHCTCPCP- - - - - 247
Db 241 KTHCTCPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDG 300

Qy 248 - - - - - G 248
Db 301 VEHNNAKTPREEQYNSTYRVVSVLTVLHQDLNMGKEYKCRVSNKALPAPIEKTISKAKG 360

Qy 249 QRPQVYTLPPSRDELTKNQVSLTCLVKGYFDPDSIAEWESNGQPENNYKTTPVLDSD 308
Db 361 QRPQVYTLPPSRDELTKNQVSLTCLVKGYFDPDSIAEWESNGQPENNYKTTPVLDSD 420

Qy 309 GSPFLYSKLTVDKSRWQQGNVFCSSVMHEALHNHYTOKLSLSLSPGK 354
Db 421 GSPFLYSKLTVDKSRWQQGNVFCSSVMHEALHNHYTOKLSLSLSPGK 466
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RESULT 12
Q6PI81 PRELIMINARY; PRT; 478 AA.
AC Q6PI81;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Primary B-Cells;
RC MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,
RA Borak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Souffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Kryzyski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP TISSUE=Primary B-Cells;
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
EMBL: BC041037; AHA41037.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00407; IGcl; 3.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 478 AA; 52666 MW; 17BED38D917970D6 CRC64;

Query Match 75.2%; Score 1410; DB 2; Length 478;
Best Local Similarity 57.7%; Pred. No. 1.6e-92;
Matches 276; Conservative 34; Mismatches 44; Indels 124; Gaps 2;

Qy 1 MGWLLILFLVAVATRVLSQVQLVQSGAEVYVKPGASVKISKASGYTFTDTHAIHWKQNP 60
Db 1 MELGLSWFLVAILEGVQCEIQLVQSGGLVQPGSLRLSCAASGFTFSYVMSWVRQAP 60

Qy 61 GQRLWICYSPGNDDFKYNRPFGKATLTADTSASTAYVELSLRSEDATVYCTSLN 120
Db 61 GKGLWVANSIKDQSEKTYVDSVKGRTFTISRDNAKNSLYLQMSLRAEDTAVYICAREFE 120

Qy 121 -----MAYWGQGLTVTVSSASTKGPSVFPFLAPSSTSGGTAAALGCLVKDY 166
Db 121 STMTVTNADYFYFYNDVWGKGTITVTVSSASTKGPSVFPFLAPSSTSGGTAAALGCLVKDY 180

Query Match 75.0%; Score 1407.5; DB 2; Length 473;
Best Local Similarity 57.9%; Pred. No. 2.3e-92;
Matches 274; Conservative 36; Mismatches 44; Indels 119; Gaps 2;

Qy 1 MGWLLILFLVAVATRVLSQVQLVQSGAEVYVKPGASVKISKASGYTFTDTHAIHWKQNP 60
Db 1 MELGLCWFLVAILEGVQCEIQLVQSGGLVQPGSLRLSCAASGFTFSFPMWVRQAP 60

Qy 61 GQRLWICYSPGNDDFKYNRPFGKATLTADTSASTAYVELSLRSEDATVYCTSLN 120
Db 61 GKGLWLSYITRSNGTIVYADSLQGRFTISRDNAKNSLYLQMSLRAEDTAVYICARQNE 120

Qy 121 -----MAYWGQGLTVTVSSASTKGPSVFPFLAPSSTSGGTAAALGCLVKDY 171
Db 121 HTSPWYSPFDYWGQGLITVTVSSASTKGPSVFPFLAPSSTSGGTAAALGCLVKDY 180

```

Query Match	74.7%;	Score	1402;	DB 2;	Length	480;			
Best Local Similarity	58.4%;	Pred. NO.	5.9e-92;						
Matches	277;	Conservative	32;	Mismatches	37;	Indels	128;	Gaps	4
Qy	8	LFLVAVATFLVSQVLVOSGAEVVKPGASVKISCKASYTFTHAIHWKQNGQGLEWI	67						
Db	8	VLLVAILKGVCHEELVELSGGGLVKPGESLRLSCAASGFTFRSFNMWVRQAPGKGLEWI	67						
Qy	68	GYF-SPGNDDFKYNRFKGAATLTADTSASTAYVELSLRSEDTAVVCFTRSLNMAI---	123						
Db	68	AFINSRGNEKY-YGSEVKGRTTISPDNADNSLFLQMSLAVDDTAIYYCARGKVVPGFT	126						
Qy	124	-----WGQGLTLTVSSASTKGPSPVFLAPSSKSTGGTAAIGCLVKDYFPP	170						
Db	127	STSGPVRHNVFDPWCGQGLTVTISASTKGPSPVFLAPSSKSTGGTAAIGCLVKDYFPP	186						

Query Match	74.6%	Score 1400;	DB 2;	Length 482;
Best Local Similarity	57.3%;	Pred. No. 8.2e-92;		
Matches	276;	Conservative	32;	Mismatches 46;
			Indels	128;
			Gaps	2
Qy	1	MGSLILLFLVAVATRVLSQVQLVQSGAEVVPKQASVKISCKASGYFTDTHAIHWKNP	60	
Db	1	MEFGLTWFFVALLRGVQCAQVVSQSGSVVQGRSURLSCIASGFFSGSAMWLRIP	60	
Qy	61	GORLEWIGYFSPGNDDPKYNERFKGKATLTADTASTAYVELSLRSGEDTAYVFCETRSLN	120	
Db	61	GKGLEWAVVISYDGNHKLKLYSDSVKGRFTI SRDNSKSLFLFLHVNLSLTADTAIYYCARDFH	120	
Qy	121	-----MAYWGQGLTVTVSSASTKGPSVPFLAPSSKTSGGTAALGCL	162	
Db	121	SKTTSIRGLPLFPYYSAMDTWGRGTTVIYSSASTKGPSVPFLAPSSKTSGGTAALGCL	180	
Qy	163	VKDYFPFPVTVSNWSGALTSGVHTFFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHK	222	
Db	181	VKDYFPFPVTVSNWSGALTSGVHTFFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHK	240	

Qy	223	PSNTKVDKKEPKSCDKTHTCPPCP	-----	247
Db	241	PSNTKVDKKEPKSCDKTHTCPPCP	PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVWD	300
Qy	248	-----	-----	247
Db	301	VSHEDPEVKFNWYVDGVEVHNAKTPREOYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN		360
Qy	248	-----	-----	292
Db	361	KALPAPIEKTISKAKGQPREPOVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG		420
Qy	293	QPENNYKTPPVLDSDGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSP		352
Db	421	QPENNYKTPPVLDSDGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSP		480
Qy	353	GK 354		
Db	481	GK 482		

Search completed: March 23, 2005, 18:30:44
Job time : 144.475 secs

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OM protein - protein search, using sw model

Run on: March 23, 2005, 18:07:03 ; Search time 94.5455 Seconds
(without alignments)
981.776 Million cell updates/sec

Title: US-10-058-069-9
Perfect score: 1243
Sequence: 1 MDSQAQVIMLLLLWVSGTCG.....EVTHQGLSSPVTKSFNRGEC 240

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_16Dec04:.*
1: geneseqp1980s:.*
2: geneseqp1990s:.*
3: geneseqp2000s:.*
4: geneseqp2001s:.*
5: geneseqp2002s:.*
6: geneseqp2003as:.*
7: geneseqp2003bs:.*
8: geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1243	100.0	240	5	Aae27927 Human CC4
2	1243	100.0	240	6	Abb82836 Antibody
3	1166	93.8	240	2	Aay50156 Chimeric
4	1136	91.4	240	2	Aay50161 Human res
5	1125	90.5	240	4	Aau00815 Human Imm
6	1122	90.3	240	8	Adj65029 Plasmid D
7	1120.5	90.1	241	2	Aar28809 Vector pM
8	1090	87.7	244	3	Aay96305 Human IGF
9	1082	87.0	220	8	Adk52314 Human ant
10	1072.5	86.3	238	8	Adl23055 Humanised
11	1072.5	86.3	238	8	Adk52304 Humanised
12	1070	85.1	220	2	Aay50172 Antibody
13	1064	85.6	220	2	Aaw07528 Anti-HGF
14	1064	85.6	220	8	Adk52386 Human ant
15	1063	85.5	220	8	Adk52334 Human ant
16	1059	85.2	220	8	Adk52362 Human ant
17	1054	84.8	220	8	Adk52298 Human ant
18	1048	84.3	220	2	Aay08601 Jp1112785
19	1044	84.0	242	4	Aau800338 Human ml
20	1044	84.0	242	4	Aau97949 HMG1 Fab
21	1044	84.0	242	4	Aau80039 HMG1 Fab
22	1040	83.7	238	6	Ada47330 TRX1 ligh
23	1040	83.7	238	6	Ada47332 TRX1 ligh
24	1040	83.7	238	8	Adp88450 Antibody
25	1040	83.7	238	8	Adp88426 Antibody

26	1040	83.7	238	8	Adq87976	Adq87976 Light cha
27	1040	83.7	238	8	Adq87964	Adq87964 Light cha
28	1034.5	83.2	238	8	Adl23052	Adl23052 Mouse/hum
29	1034.5	83.2	238	8	AdS88793	AdS88793 A mouse/h
30	1030	82.9	238	6	ADA47339	Ada47339 TRX1 ligh
31	1030	82.9	238	6	ADA47338	Ada47338 TRX1 ligh
32	1030	82.9	238	8	ADP88434	Adp88434 Antibody
33	1030	82.9	238	8	ADP88442	Adp88442 Antibody
34	1030	82.9	238	8	Adq87972	Adq87972 Light cha
35	1030	82.9	238	8	Adq87968	Adq87968 Light cha
36	1019.5	82.0	239	3	AB03697	AB03697 Immunoglo
37	1019.5	82.0	239	7	ADb72862	Adb72862 Human AAA
38	1014.5	81.6	238	5	ABG70744	Abg70744 Mouse/hum
39	1004.5	80.8	238	7	ADe64203	AdE64203 LL2LC pro
40	1001	80.5	234	8	ADR72766	Adr72766 Human mon
41	998.5	80.3	237	2	AAW73873	Aaw73873 Human ant
42	997.5	80.2	235	6	ABP71366	Abp71366 Anti-OPGL
43	997	80.2	238	3	AAW90931	Aaw90931 Humanised
44	997	80.2	238	5	ABb74900	Abb74900 Humanised
45	996	80.1	234	3	AAy92239	Aay92239 Human bon

ALIGNMENTS

RESULT 1						
AAE27927						
ID	AAE27927 standard; protein; 240 AA.					
XX						
AC	AAE27927;					
XX						
DT	27-DEC-2002 (first entry)					
XX						
DE	Human CC49 antibody light chain protein.					
XX						
KW	Human; CC49 antibody; C2B8 antibody; tumour associated antigen; TAG-72;					
KW	neoplasm; neoplastic disorder; haematologic neoplasm; colon cancer;					
KW	non-Hodgkin's lymphoma; haematologic malignancy; tumour.					
XX						
OS	Homo sapiens.					
XX						
PN	WO200260955-A2.					
XX						
PD	08-AUG-2002.					
XX						
PF	29-JAN-2002; 2002WO-US002373.					
XX						
PR	29-JAN-2001; 2001US-0264318P.					
XX						
PA	16-NOV-2001; 2001US-0331481P.					
XX						
PI	(IDEC-) IDEC PHARM CORP.					
XX						
PI	Braslawsky GR, Hanna N, Chinn P;					
XX						
DR	WPI; 2002-698547/75.					
XX						
DR	N-PSDB; AAD45756.					
XX						
PT	Novel domain deleted CC49 antibody reactive with tumor associated antigen					
XX						
PT	-72, or C2B8 antibody reactive with CD20, useful for treating					
XX						
XX	myelosuppressed patient suffering from a neoplastic disorder.					
XX						
PS	Example 1; Fig 5A; 74pp; English.					
XX						
CC	The present invention relates to domain deleted CC49 or C2B8 antibodies.					
XX						
CC	Domain deleted CC49 antibodies comprise a heavy chain human CC49 domain					
XX						
CC	deleted sequence in which CH2 domain has been deleted and are reactive					
XX						
CC	with tumour associated antigen (TAG)-72. The C2B8 antibodies are reactive					
XX						
CC	domain deleted C2B8 construct where the CH2 domain has been deleted.					
XX						
CC	Sequences of the invention are useful for imaging a neoplasm. They are					
XX						
CC	also useful for treating myelosuppressed patients suffering from					
XX						
CC	neoplastic disorder such as haematologic neoplasm, preferably non-					
XX						
CC	Hodgkin's lymphoma. Antibodies of the invention are also used to treat					

CC neoplastic disorder, colon cancer and haematologic malignancy. They are
 CC useful for reducing tumour size, inhibiting tumour growth and/or
 CC prolonging the survival time of tumour-bearing animals and for treating
 CC tumours. The present sequence is human CC49 light chain protein. This
 CC sequence is used in the exemplification of the invention
 XX
 XX Sequence 240 AA;

Query Match 100.0%; Score 1243; DB 5; Length 240;
 Best Local Similarity 100.0%; Pred. No. 3.8e-67;
 Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDSQAQVLMILLWVSGTCGDIWMSQSPDSLAVSLGERVTINCKSSQSLLYSGNQKNYLA 60
 DB 1 MDSQAQVLMILLWVSGTCGDIWMSQSPDSLAVSLGERVTINCKSSQSLLYSGNQKNYLA 60
 QY 61 WYQKPGQSPKLLIYWASARESGVDPDRFSGSGSGTDFLTITSSVQAEADVAVVYCCQYYSY 120
 DB 61 WYQKPGQSPKLLIYWASARESGVDPDRFSGSGSGTDFLTITSSVQAEADVAVVYCCQYYSY 120
 QY 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCILNPFYPREAKVQWKVDNAL 180
 DB 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCILNPFYPREAKVQWKVDNAL 180
 QY 181 QSGNSQESVTEQDSKDSYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 240
 DB 181 QSGNSQESVTEQDSKDSYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 240

RESULT 2
 ABB82836
 ID ABB82836 standard; protein; 240 AA.

AC ABB82836;
 XX
 XX
 DT 31-MAR-2003 (first entry)
 XX
 DE Antibody huCC49 light chain.
 XX
 CC49; antibody; cytostatic; antiallergic; antianemic; antiasthmatic;
 KW vsotropic; immunomodulator; protozoacide; antidiabetic; nephrotropic;
 KW thymimetic; hepatotropic; haemostatic; antileprotic; antibacterial;
 KW neuroprotective; antipneumatic; antirheumatic; antiarthritic; antiulcer;
 KW dermatological; immunosuppressive; antiinflammatory.
 XX
 OS Homo sapiens.
 XX
 XX WO200296948-A2.
 XX
 PD 05-DEC-2002.
 XX
 XX 29-JAN-2002; 2002WO-US002374.
 XX
 PR 29-JAN-2001; 2001US-0264319P.
 FR 16-NOV-2001; 2001US-0331481P.
 PR 21-DEC-2001; 2001US-0341859P.
 XX
 XX (IDEC-) IDEC PHARM CORP.
 XX
 XX Braslawsky GR, Hanna N, Chinn P, Hariharan K;
 XX WPI; 2003-140446/13.
 DR N-PSDB; ABZ24020.
 XX
 XX Novel dimeric antibody useful for treating immune disorder and neoplastic
 PT disorder, has several non-covalently associated monomeric subunits.
 XX
 XX Example 1; Fig 5A; 78pp; English.
 PS
 XX The invention relates to a dimeric antibody (I) comprising several
 CC monomeric subunits, where the monomeric subunits are non-covalently
 CC associated. (I) is useful for treating a disorder, especially immune
 CC disorder, and neoplastic disorder such as relapsed Hodgkin's disease,

CC resistant Hodgkin's disease high grade, low grade and intermediate grade
 CC non-Hodgkin's lymphomas, B cell chronic lymphocytic leukemia (B-CLL),
 CC lymphoplasmacytoid lymphoma (LPL), mantle cell lymphoma (MCL), follicular
 CC lymphoma (FL), diffuse large cell lymphoma (DLCL), Burkitt's lymphoma,
 CC AIDS-related lymphomas, monocytic B cell lymphoma, angioimmunoblastic
 CC lymphadenopathy, small lymphocytic, follicular, diffuse large cell,
 CC diffuse small cleaved cell, large cell immunoblastic lymphoblastoma,
 CC small, non-cleaved, Burkitt's and non-Burkitt's, follicular, mixed small
 CC cleaved and large cell lymphomas, in a mammal (see ABZ24017 for a
 CC detailed description of the various uses of (I)). The present sequence
 CC represents the antibody huCC49 light chain
 XX
 XX Sequence 240 AA;

Query Match 100.0%; Score 1243; DB 6; Length 240;
 Best Local Similarity 100.0%; Pred. No. 3.8e-67;
 Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDSQAQVLMILLWVSGTCGDIWMSQSPDSLAVSLGERVTINCKSSQSLLYSGNQKNYLA 60
 DB 1 MDSQAQVLMILLWVSGTCGDIWMSQSPDSLAVSLGERVTINCKSSQSLLYSGNQKNYLA 60
 QY 61 WYQKPGQSPKLLIYWASARESGVDPDRFSGSGSGTDFLTITSSVQAEADVAVVYCCQYYSY 120
 DB 61 WYQKPGQSPKLLIYWASARESGVDPDRFSGSGSGTDFLTITSSVQAEADVAVVYCCQYYSY 120
 QY 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCILNPFYPREAKVQWKVDNAL 180
 DB 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCILNPFYPREAKVQWKVDNAL 180
 QY 181 QSGNSQESVTEQDSKDSYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 240
 DB 181 QSGNSQESVTEQDSKDSYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 240

RESULT 3
 AAY50156
 ID AAY50156 standard; protein; 240 AA.

XX AAY50156;
 XX
 DT 17-OCT-2003 (revised)
 DT 31-JAN-2000 (first entry)
 XX
 DE Chimeric mouse/human F19 antibody light chain.
 XX
 KW Antibody; monoclonal; F19; fibrinogen activation protein alpha; FAP;
 KW humanisation; complementarity determining region; CDR; CDR grafting;
 KW reactive stroma; fibroblast; epithelial cancer; diagnosis;
 KW immune response; framework sequence; constant region; variable region;
 KW producibility; treatment; cancer; colorectal; lung; breast; head; neck;
 KW ovarian; lung; bladder; pancreatic; metastasis; detection; wound healing;
 KW skin inflammation; tumour; immunogenicity; chimeric; light chain.
 XX
 OS Mus sp.
 OS Homo sapiens.
 OS Chimeric.
 XX
 XX Location/Qualifiers
 FT Peptide 1..20 /note= "Leader peptide"
 FT Protein 21..240 /note= "Mature chimeric mouse/human F19 light chain"
 FT Region 21..140 /note= "Mature mouse F19 light chain variable region"
 FT Region 44..60 /note= "Complementarity determining region (CDR) 1"
 FT Region 76..82 /note= "CDR 2"
 FT Region 115..123 /note= "CDR 3"
 FT Region 141..240 /note= "Human kappa light chain constant region"

XX EP953639-A1.
 PN
 XX 03-NOV-1999.
 PD
 XX 30-APR-1998; 98EP-00107925.
 PF
 XX 30-APR-1998; 98EP-00107925.
 PR
 XX (BOEH) BOEHRINGER INGELHEIM INT GMBH.
 PA
 PI Park JE, Garin-Chesa P, Bamberger U, Leger O, Saldanha J;
 PI Rettig WJ;
 PI WPI: 1999-621833/54.
 DR N-PSDB; AAZ32781.
 DR
 XX New antibody protein, useful for treating cancer and for imaging presence
 PT of activated stromal fibroblasts in healing wound or inflamed skin.
 PT
 XX Example 1; Fig 26; 143pp; English.
 PS
 XX This sequence represents the light chain of a chimeric mouse/human F19
 CC antibody. F19 (ATCC Accession number HB 8269) is a murine monoclonal
 CC antibody against fibroblast activation protein alpha (FAP). FAP is a cell
 CC surface molecule of reactive stromal fibroblasts, and its induction is a
 CC highly consistent molecular trait of the reactive stroma of many types of
 CC epithelial cancer. Although F19 may be useful in vitro, e.g., for
 CC diagnosis, its applications for in vivo use in humans are problematic as
 CC it elicits a human anti-mouse response which reduces the efficacy of the
 CC antibody in patients and impairs continued administration. This chimeric
 CC antibody was humanised by joining entire murine variable regions to human
 CC constant regions. However, humanised antibodies produced by this method
 CC can still elicit an anti-mouse response in humans, whereas antibodies
 CC humanised via CDR (complementarity determining region) grafting are less
 CC immunogenic in humans. Humanised F19 antibodies are useful for treating
 CC cancers e.g., colorectal cancers, non-small cell lung cancers, breast
 CC cancers, head and neck cancers, ovarian cancers, lung cancers, bladder
 CC cancers, pancreatic cancers and metastatic cancers. They are also useful
 CC for the detection of activated stromal fibroblasts in a healing wound,
 CC inflamed skin or a tumour in a human patient. (Updated on 17-OCT-2003 to
 CC standardise OS field)
 XX
 XX Sequence 240 AA;
 SQ

Query Match 93.8%; Score 1166; DB 2; Length 240;
 Best Local Similarity 93.3%; Pred. No. 1.6e-62;
 Matches 224; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MDSQAVLMLLLWVSGTGGDIVMSQSPDSLAVSLGERVTNLCKSSQSLLYSGNQKNYLA 60
 Db 1 MDSQAVLMLLLWVSGTGGDIVMSQSPDSLAVSLGERVTNLCKSSQSLLYSGNQKNYLA 60
 Qy 61 WYQKPGOSPKLLIYVWASARESGVDPDRSGSGTDFTLTSSVQAEADVAVVYCOQYYSY 120
 Db 61 WYQKPGOSPKLLIYVWASARESGVDPDRSGSGTDFTLTSSVQAEADVAVVYCOQYYSY 120
 Qy 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL 180
 Db 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL 180
 Qy 181 QSGNSQESVTPQDSKDSYISLSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 240
 Db 181 QSGNSQESVTPQDSKDSYISLSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 240

RESULT 4
 AAY50161
 ID AAY50161 standard; protein; 240 AA.
 XX
 XX AAY50161;
 AC
 XX 17-OCT-2003 (revised)
 DT

DT 31-JAN-2000 (first entry)
 XX Human reshaped F19 antibody light chain (version a).
 DE
 XX Antibody; monoclonal; F19; fibrinogen activation protein alpha; FAP;
 KW humanisation; complementarity determining region; CDR; CDR grafting;
 KW reshaped; reactive stroma; fibroblast; epithelial cancer; diagnosis;
 KW immune response; framework sequence; constant region; variable region;
 KW producibility; treatment; cancer; colorectal; lung; breast; head; neck;
 KW ovarian; lung; bladder; pancreatic; metastasis; detection; wound healing;
 KW skin inflammation; tumour; immunogenicity; chimeric; light chain.
 XX
 OS Mus sp.
 OS Homo sapiens.
 OS Chimeric.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..20 "Leader peptide"
 FT Protein 21..240
 FT Region 21..140
 FT /note= "Mature human reshaped F19 light chain variable
 FT region"
 FT Region 44..60
 FT /note= "Complementarity determining region (CDR) 1"
 FT Region 76..82
 FT /note= "CDR 2"
 FT Region 115..123
 FT /note= "CDR 3"
 FT Region 141..240
 FT /note= "Human kappa light chain constant region"
 XX EP953639-A1.
 XX 03-NOV-1999.
 XX 30-APR-1998; 98EP-00107925.
 XX 30-APR-1998; 98EP-00107925.
 XX (BOEH) BOEHRINGER INGELHEIM INT GMBH.
 XX Park JE, Garin-Chesa P, Bamberger U, Leger O, Saldanha J;
 XX Rettig WJ;
 XX WPI: 1999-621833/54.
 XX N-PSDB; AAZ32784.
 XX New antibody protein, useful for treating cancer and for imaging presence
 XX of activated stromal fibroblasts in healing wound or inflamed skin.
 XX Example 3; Fig 30; 143pp; English.
 XX This sequence represents the light chain (version a) of a reshaped human
 XX F19 antibody. F19 (ATCC Accession number HB 8269) is a murine monoclonal
 XX antibody against fibroblast activation protein alpha (FAP). FAP is a cell
 XX surface molecule of reactive stromal fibroblasts, and its induction is a
 XX highly consistent molecular trait of the reactive stroma of many types of
 XX epithelial cancer. Although F19 may be useful in vitro, e.g., for
 XX diagnosis, its applications for in vivo use in humans are problematic as
 XX it elicits a human anti-mouse response which reduces the efficacy of the
 XX antibody in patients and impairs continued administration. The novel
 XX human reshaped F19 was humanised by grafting the murine complementarity
 XX determining regions (CDRs) of F19 onto human variable region framework
 XX sequences, and then joining these "reshaped human" variable regions to
 XX human constant regions. These modifications also result in the improved
 XX producibility in eukaryotic cell culture systems as compared to a
 XX chimeric antibody having the entire variable regions of F19 joined to
 XX human constant regions. The human reshaped F19 antibody has low
 XX immunogenicity for humans and is useful for treating cancers e.g.,
 XX colorectal cancers, non-small cell lung cancers, breast cancers, head and
 XX neck cancers, ovarian cancers, lung cancers, bladder cancers, pancreatic

Db 7 AQLGLLLWLPARGDVTMTQSPDLSVLSGERATINCKSGSLLYSTNQKYLAWYQQ 66
 Qy 65 KPGQPKLLIYWASAREGVDPFRFSGSGGTDFTLTISVQAEADVAVYCCQYYSYPLTF 124
 Db 67 KPGQPKLLIYWASAREGVDPFRFSGSGGTDFTLTISVQAEADVAVYCCQYYSY-RTF 125
 Qy 125 GAGTKLEIKRTVAAPSVFIFFPSDQLKSGTASVCLLNFPYPRKAVQWVDNALQSGN 184
 Db 126 GRGTKLEIKRTVAAPSVFIFFPSDQLKSGTASVCLLNFPYPRKAVQWVDNALQSGN 185
 Qy 185 SQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
 Db 186 SQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 241

RESULT 8

AA96305
 ID AA96305 standard; protein; 244 AA.

AC AA96305;

DT 16-AUG-2000 (first entry)

DE Human IGFAM-17 immunoglobulin.

XX Human; immunoglobulin; IGFAM-17; IGFAM; immune disorder; cancer;
 KW infection; inflammation; haematopoiesis; AIDS; allergy.

OS Homo sapiens.

XX Key Location/Qualifiers
 FH Peptide 1..20
 FT /label= signal_peptide
 FT Protein 21..244
 FT /label= IGFAM-17
 FT Domain 40..120
 FT /label= Ig_domain
 FT Domain 157..226
 FT /label= Ig_domain

XX WO200029583-A2.

XX 25-MAY-2000.

XX 19-NOV-1999; 99WO-US027566.

XX 19-NOV-1998; 98US-00195853.

XX 22-DEC-1998; 98US-0113635P.

XX 07-APR-1999; 99US-0128194P.

XX (INCY-) INCYTE PHARM INC.

XX Yue H, Tang YT, Corley NC, Guegler KJ, Gorgone GA, Baughn MR;
 PI Lu DAM, Lal P, Hillman JL, Yang J;

XX WPI; 2000-387796/33.

XX N-PSDB; AAA27397.

XX Immunoglobulin superfamily proteins, the agonist and antagonist of the
 PT protein is useful for preventing and treating disorders associated with
 PT altered levels of the protein such as cancer, immune system disorders.

XX Claim 1; Page 91-92; 105pp; English.

XX The present sequence is the human immunoglobulin superfamily protein
 CC IGFAM-17. Its gene was isolated from a cDNA library of intestine tissue.
 CC It is expressed in reproductive, gastrointestinal, immune and
 CC haematopoietic and cardiovascular tissue, where cancer and inflammation
 CC are common. The gene, protein, its antibodies, agonists and antagonists
 CC are suitable for diagnosing and treating many diseases, including cancer,
 CC immune system disorders (such as inflammation, AIDS, allergies, anaemia,
 CC arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's
 CC disease, diabetes mellitus, emphysema, Graves' disease, hepatitis,

CC multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma,
 CC systemic lupus erythematosus and ulcerative colitis), complications of
 CC cancer, haemodialysis and extracorporeal circulation, trauma and
 CC haematopoietic cancer (such as leukaemia) and infections caused by
 CC bacteria, viruses, fungi or parasites
 XX Sequence 244 AA;

Query Match 87.7%; Score 1090; DB 3; Length 244;
 Best Local Similarity 85.9%; Pred. No. 5.8e-58;
 Matches 207; Conservative 14; Mismatches 16; Indels 4; Gaps 1;

Qy 4 QAQVLMILLWVS-----GTGCDIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKNYL 59
 Db 4 QTQVFISILLWISVLTAGAYGDIWMTQSPDLSVLSGERATITCKSSQSVFYNNKNYL 63

Qy 60 AWYQKPGQPKLLIYWASAREGVDPFRFSGSGGTDFTLTISVQAEADVAVYCCQYYS 119

Db 64 VWYQKPGQPKLLIYWASAREGVDPFRFSGSGGTDFTLTISVQAEADVAVYCCQYYS 123

Qy 120 YPLTFGAGTKLEIKRTVAAPSVFIFFPSDQLKSGTASVCLLNFPYPRKAVQWVDNA 179

Db 124 TPYTFGQGTREIKRTVAAPSVFIFFPSDQLKSGTASVCLLNFPYPRKAVQWVDNA 183

Qy 180 LQSGNSQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGE 239

Db 184 LQSGNSQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGE 243

Qy 240 C 240

Db 244 C 244

RESULT 9

ID ADK52314 standard; protein; 220 AA.

XX ADK52314;

XX 20-MAY-2004 (first entry)

DE Human anti-MCP-1 variable region light chain #5.

XX monocyte chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;
 KW Antirheumatic; Nephrotropic; Antiarteriosclerotic; Antipsoriatic;
 KW Vasotropic; Immunosuppressive; Neuroprotective; neoplastic;
 KW inflammatory condition; cancer; arthritis; multiple sclerosis;
 XX anti-MCP-1; heavy chain; light chain.

OS Homo sapiens.

XX WO2004016769-A2.

XX 26-FEB-2004.

XX 19-AUG-2003; 2003WO-US026232.

XX 19-AUG-2002; 2002US-0404802P.

XX (ABGE-) ABGENIX INC.

XX Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;
 PI Bhakta S;

XX WPI; 2004-203794/19.

XX N-PSDB; ADK52313.

XX New human monoclonal antibody that binds to monocyte chemo-attractant
 CC protein-1 and is immobilized on an insoluble matrix, useful for
 CC diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,
 CC rheumatoid arthritis or psoriasis.

XX Claim 2; SEQ ID NO 20; 154pp; English.

```
XX CC The present invention relates to a human monoclonal antibody that binds
CC to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful
CC for the preparation of a medicament useful for treating neoplastic or
CC inflammatory conditions. The neoplastic disease is selected from breast
CC cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC pancreatic cancer or prostate cancer. The inflammatory condition is
CC selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,
CC psoriasis, restenosis, autoimmune disease or multiple sclerosis. The
CC antibodies are also useful for diagnosing the above diseases. It is also
CC useful for the determining the level of MCP-1 and MCP-1 family members in
CC patient samples. The present sequence represents a human anti-MCP-1
CC variable region light chain sequence.
XX SQ Sequence 220 AA;
      Query Match      87.0%; Score 1082; DB 8; Length 220;
      Best Local Similarity 93.6%; Pred. No. 1.6e-57;
      Matches 206; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
Qy 21 DIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNKNYLAWYQKPGSPKLLIYWASAR 80
Db 1 DIVMTQSPDSLAVSLGERATINCKSSQSLYSSNNKNYLVWYQKPGQPPKLLIYWASIR 60
Qy 81 ESGVPDRFSGSGGTDTLTITSSVQAEDVAVYVCOQYYSYELTGTGCTKLEKETAAPS 140
Db 61 ESGVPDRFSGSGGTDTLTITSSVQAEDVAVYVCOQYYSYELTGTGCTKLEKETAAPS 120
Qy 141 VFIFPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQSVTEQDSKDYSTYS 200
Db 121 VFIFPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQSVTEQDSKDYSTYS 180
Qy 201 LSSLTILSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 240
Db 181 LSSLTILSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 220
      RESULT 10
      ADL23055
      ID ADL23055 standard; protein; 238 AA.
      AC ADL23055;
      DT 20-MAY-2004 (first entry)
      DE Humanised anti-MAG antibody #2.
      KW antibody; MAG; myelin associated glycoprotein; stroke;
      XX neurodegenerative disorder; gene therapy; vaccine; human.
      OS Homo sapiens.
      OS Chimeric.
      OS Unidentified.
      XX WO2004014953-A2.
      FN 19-FEB-2004.
      XX 05-AUG-2003; 2003WO-EP008749.
      XX 06-AUG-2002; 2002GB-00018229.
      PR 06-AUG-2002; 2002GB-00018230.
      PR 06-AUG-2002; 2002GB-00018232.
      PR 06-AUG-2002; 2002GB-00018234.
      XX (GLAX ) GLAXO GROUP LTD.
      PA Ellis JH, Germaschewski V;
      XX WPI; 2004-180641/17.
      DR WPI; 2004-691029/67.
      XX Promoting oligodendrocyte survival in humans with neurological diseases,
      PT such as Alzheimer's disease, multiple sclerosis and/or stroke, using an
```

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PT glycoprotein (MAG), useful for preparing a composition for treating or
PT preventing stroke or other neurodegenerative disorders e.g., Alzheimer's
PT disease.
XX Example 4; Fig 5; 67pp; English.
XX The present invention relates to a new altered antibody or its functional
CC fragment, which binds to and neutralizes myelin associated glycoprotein
CC (MAG) and comprises a light chain variable domain (VL) comprising
CC complementary determining region light 1 (CDRL1), CDRL2 or CDRL3 and/or a
CC heavy chain variable domain (VH) comprising CDRH1, CDRH2 or CDRH3. The
CC antibody is useful for preparing a composition for treating or preventing
CC stroke or other neurodegenerative disorders in a human, e.g., traumatic
CC brain injury, Alzheimer's disease, dementias, peripheral neuropathy,
CC Parkinson's disease, Huntington's disease and multiple sclerosis. The
CC present sequence is a humanised anti-MAG antibody.
XX SQ Sequence 238 AA;
      Query Match      86.3%; Score 1072.5; DB 8; Length 238;
      Best Local Similarity 88.5%; Pred. No. 6.4e-57;
      Matches 207; Conservative 10; Mismatches 16; Indels 1; Gaps 1;
Qy 7 VLMLLILVWVGTCGDIIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNKNYLAWYQK 66
Db 6 IILFLVATATGVHSDIIVMTQSPDSLAVSLGERATINCKSSHSVLYSSNNKNYLAWYQK 65
Qy 67 GQSPKLLIYWASARESVPDRFSGSGGTDTLTITSSVQAEDVAVYVCOQYYSYELTGTG 126
Db 66 GQSPKLLIYWASTRESGVPDRFSGSGGTDTLTITSSVQAEDVAVYVCOQYYSYELTGTG 124
Qy 127 GTKLELKRVTAAAPSVFIPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ 186
Db 125 GTKLEIKRTVAAPSVFIPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ 184
Qy 187 ESVTEQDSKDYSTYLSLTILSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 240
Db 185 ESVTEQDSKDYSTYLSLTILSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 238
      RESULT 11
      ADS88804
      ID ADS88804 standard; protein; 238 AA.
      AC ADS88804;
      DT 16-DEC-2004 (first entry)
      DE Humanised anti-MAG antibody light chain.
      KW oligodendrocyte; stroke; neurological disease;
      KW myelin-associated glycoprotein; MAG; anti-MAG antibody;
      XX Alzheimer's disease; multiple sclerosis.
      OS Homo sapiens.
      OS Synthetic.
      XX WO2004083363-A2.
      FN 30-SEP-2004.
      XX 02-FEB-2004; 2004WO-EP001016.
      XX 19-MAR-2003; 2003GB-00006309.
      XX (GLAX ) GLAXO GROUP LTD.
      XX Vinson M, Irving EA;
      XX WPI; 2004-691029/67.
      XX Promoting oligodendrocyte survival in humans with neurological diseases,
      PT such as Alzheimer's disease, multiple sclerosis and/or stroke, using an
```

PT anti-myelin-associated glycoprotein (MAG) antibody.

PS Claim 18; SEQ ID NO 19; 45pp; English.

XX The specification describes a method for promoting oligodendrocyte survival in a human suffering or at risk of developing stroke or another neurological disease. The method comprises administering to the human an anti-myelin-associated glycoprotein (MAG) antibody or its functional fragment. The anti-MAG antibody or its functional fragment is useful in the manufacture of a medicament for the promotion of oligodendrocyte survival in a human suffering from or at risk of developing stroke or another neurological disease. They can also be used in treating neurological diseases, such as Alzheimer's disease, multiple sclerosis and/or stroke, by promoting oligodendrocyte survival. The present sequence represents a humanised immunoglobulin light chain in which the humanised anti-MAG light chain variable region is associated with a functional immunoglobulin secretion signal sequence, and with the human kappa constant region. Antibodies used in the method of the invention may comprise the present heavy chain.

XX Sequence 238 AA;

Query Match 86.3%; Score 1072.5; DB 8; Length 238;

Best Local Similarity 88.5%; Pred. No. 6.4e-57; Mismatches 10; Indels 1; Gaps 1;

Matches 207; Conservative 10; Mismatches 16; Indels 1; Gaps 1;

QY 7 VLMLLLVSGTCGDIVMSQSPDSILAVSLGSRVTINCKSSQSLYSNGKNLYAWYQOKP 66

Db 6 IILFLVATATGVHSDIVMTQSPDSLAVSLGERATINCKSSHSVLYSSNQKNLYAWYQOKP 65

QY 67 GQSPKLLIYASARESGVDFRPSGSGTDTLTISVQAEADVAVYVCOQYYSPLTFGA 126

Db 66 GQPPKLLIYASTRESGVDFRPSGSGTDTLTISVQAEADVAVYVCHOYLS-SLTFGQ 124

QY 127 GTKLEKRTVAAPSVFIIPPDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQ 186

Db 125 GTKLEKRTVAAPSVFIIPPDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQ 184

QY 187 ESVTEQDSKSTYSLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNREGC 240

Db 185 ESVTEQDSKSTYSLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNREGC 238

RESULT 12

ID AAY50172 standard; protein; 220 AA.

XX AC AAY50172;

DT 17-OCT-2003 (revised)

XX 31-JAN-2000 (first entry)

DE Antibody F19 chimeric mouse/human light chain variable region (chF19LC).

XX Antibody; monoclonal; F19; fibrinogen activation protein alpha; FAP; humanisation; complementarity determining region; CDR; CDR grafting; reactive stroma; fibroblast; epithelial cancer; diagnosis; immune response; framework sequence; constant region; variable region; producibility; treatment; cancer; colorectal; lung; breast; head; neck; ovarian; lung; bladder; pancreatic; metastasis; detection; wound healing; skin inflammation; tumour; immunogenicity; chimeric; light chain.

XX Mus sp.

OS Homo sapiens.

OS Chimeric.

XX EP953639-A1.

XX 03-NOV-1999.

XX 30-APR-1998; 98EP-00107925.

XX 30-APR-1998; 98EP-00107925.

XX (BOEH) BOEHRINGER INGELHEIM INT GMBH.

PI Park JB, Garin-Chesa P, Bamberger U, Leger O, Saldanha J; Rettig WJ;

XX WPI; 1999-621833/54.

XX New antibody protein, useful for treating cancer and for imaging presence of activated stromal fibroblasts in healing wound or inflamed skin.

XX Example 1; Fig 17; 143pp; English.

XX This sequence represents the light chain variable region of a chimeric mouse/human F19 antibody (chF19LC). F19 (ATCC Accession number HB 8269) is a murine monoclonal antibody against fibroblast activation protein alpha (FAP). FAP is a cell surface molecule of reactive stromal fibroblasts, and its induction is a highly consistent molecular trait of the reactive stroma of many types of epithelial cancer. Although F19 may be useful in vitro, e.g., for diagnosis, its applications for in vivo use in humans are problematic as it elicits a human anti-mouse response which reduces the efficacy of the antibody in patients and impairs continued administration. This chimeric antibody was humanised by joining entire murine variable regions to human constant regions. However, humanised antibodies produced by this method can still elicit an anti-mouse response in humans, whereas antibodies humanised via CDR (complementarity determining region) grafting are less immunogenic in humans. Humanised F19 antibodies are useful for treating cancers e.g., colorectal cancers, non-small cell lung cancers, breast cancers, head and neck cancers, ovarian cancers, lung cancers, bladder cancers, pancreatic cancers and metastatic cancers. They are also useful for the detection of activated stromal fibroblasts in a healing wound, inflamed skin or a tumour in a human patient. (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 220 AA;

Query Match 86.1%; Score 1070; DB 2; Length 220;

Best Local Similarity 93.2%; Pred. No. 8.4e-57;

Matches 205; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY 21 DIVMSQSPDSILAVSLGSRVTINCKSSQSLYSNGKNLYAWYQOKPQSPKLLIYASAR 80

Db 1 DIVMSQSPDSILAVSLGSRVTINCKSSQSLYSNGKNLYAWYQOKPQSPKLLIYASTR 60

QY 81 ESGVDFRPSGSGTDTLTISVQAEADVAVYVCOQYYSPLTFGAGTKLEKRTVAAPS 140

Db 61 ESGVDFRPSGSGTDTLTISVQAEADVAVYVCOQYYSPLTFGAGTKLEKRTVAAPS 120

QY 141 VFIPPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQSVTEQDSKSTYS 200

Db 121 VFIPPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQSVTEQDSKSTYS 180

QY 201 LSSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNREGC 240

Db 181 LSSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNREGC 220

RESULT 13

AAW07528

ID AAW07528 standard; protein; 220 AA.

XX AC AAW07528;

XX 04-MAR-1997 (first entry)

DE Anti-HGF receptor MAB 5D5 Fab light chain.

XX Hepatocyte growth factor receptor; HGF; c-Met; antagonist;

XX monoclonal antibody; MAb; Fab; breast cancer; pancreas cancer;

XX colon cancer; lung cancer; therapy.

XX Mus sp.

XX

PN WO9638557-A1.
 XX 05-DEC-1996.
 PD 31-MAY-1996; 96WO-US008094.
 XX 02-JUN-1995; 95US-00460368.
 PF (GETH) GENENTECH INC.
 XX Schwall RH, Tabor KH;
 XX WPI; 1997-034371/03.
 DR N-PSDB; AAT43873.
 XX Hepatocyte growth factor receptor antagonist - specifically anti-c-Met
 PT receptor monoclonal antibody 5D5 Fab, useful for mammalian cancer
 PT treatment.
 XX Claim 12; Fig 1A; 69pp; English.
 PS
 CC 5D5 Fab comprises a light chain (AAW07528) and heavy chain (AAW07529) of
 CC monoclonal antibody (Mab) 5D5, a murine Mab raised against the hepatocyte
 CC growth factor (HGF) receptor (c-Met). The Fab can be obtd. by papain
 CC digestion of the Mab or by recombinant methods utilising cDNA clones
 CC (AAT43873-74) coding for the light and heavy chains. 5D5 Fab is an
 CC antagonist of the HGF receptor and is useful for the diagnosis and
 CC treatment of breast, pancreas, colon and lung cancer
 CC
 XX Sequence 220 AA;
 SQ
 Query Match 85.6%; Score 1064; DB 2; Length 220;
 Best Local Similarity 90.9%; Pred. No. 1.9e-56;
 Matches 200; Conservative 14; Mismatches 6; Indels 0; Gaps 0;
 QY 21 DIVMSQSPDSLAVSLGERVTINCKSSQSLLYSGNQKNYLAWYQKPGQSPKLLIYWASAR 80
 DB 1 DIVMSQSPSLTVSGEKTIVTSCKSSQSLLYTSQKNYLAWYQKPGQSPKLLIYWASTR 60
 QY 81 ESGVDPFRSGSGSDFTLTITSSVOAEDVAVYVCOQYYSYPLTFGAGTKLEKRTVAAPS 140
 DB 61 ESGVDPFRSGSGSDFTLTITSVKADLAVYVCOQYVAYPWTGGTKLEIKRTVAAPS 120
 QY 141 VFIFPPSDEQLKSGTASVCLLNFPYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 200
 DB 121 VFIFPPSDEQLKSGTASVCLLNFPYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 180
 QY 201 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
 DB 181 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220
 RESULT 14
 ADK52386
 ID ADK52386 standard; protein; 220 AA.
 XX
 AC ADK52386;
 AC
 XX 20-MAY-2004 (first entry)
 DT
 XX Human anti-MCP-1 variable region light chain #23.
 DE
 XX monocyte chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;
 XX Antirheumatic; Nephrotropic; Antiartherosclerotic; Antipsoriatic;
 KW Vasotrophic; Immunosuppressive; Neuroprotective; Neoplastic;
 KW inflammatory condition; cancer; arthritis; multiple sclerosis;
 KW anti-MCP-1; heavy chain; light chain.
 XX
 OS Homo sapiens.
 XX
 XX WO2004016769-A2.
 XX
 PD 26-FEB-2004.
 XX

XX 19-AUG-2003; 2003WO-US026232.
 XX 19-AUG-2002; 2002US-0404802P.
 PR (ABGE-) ABGENIX INC.
 XX Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;
 PI Bhakta S;
 XX WPI; 2004-203794/19.
 DR N-PSDB; ADK52385.
 XX New human monoclonal antibody that binds to monocyte chemo-attractant
 PT protein-1 and is immobilized on an insoluble matrix, useful for
 PT diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,
 PT rheumatoid arthritis or psoriasis.
 XX Claim 2; SEQ ID NO 92; 154pp; English.
 PS
 CC The present invention relates to a human monoclonal antibody that binds
 CC to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful
 CC for the preparation of a medicament useful for treating neoplastic or
 CC inflammatory conditions. The neoplastic disease is selected from breast
 CC cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
 CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
 CC pancreatic cancer or prostate cancer. The inflammatory condition is
 CC selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,
 CC psoriasis, restenosis, autoimmune disease or multiple sclerosis. The
 CC antibodies are also useful for diagnosing the above diseases. It is also
 CC useful for the determining the level of MCP-1 and MCP-1 family members in
 CC patient samples. The present sequence represents a human anti-MCP-1
 CC variable region light chain sequence.
 XX Sequence 220 AA;
 SQ
 Query Match 85.6%; Score 1064; DB 8; Length 220;
 Best Local Similarity 91.8%; Pred. No. 1.9e-56;
 Matches 202; Conservative 7; Mismatches 11; Indels 0; Gaps 0;
 QY 21 DIVMSQSPDSLAVSLGERVTINCKSSQSLLYSGNQKNYLAWYQKPGQSPKLLIYWASAR 80
 DB 1 DIVMTQSPDSLAVSLGERATINCKSSQSLVSSNNKNYLVWYQKPGQPKLLIYWASTR 60
 QY 81 ESGVDPFRSGSGSDFTLTITSSVOAEDVAVYVCOQYYSYPLTFGAGTKLEKRTVAAPS 140
 DB 61 ESGVDPFRSGSGSDFTLTITSSLAQEDVGVYVCOQYVTSPTTGGTKVBIKRTVAAPS 120
 QY 141 VFIFPPSDEQLKSGTASVCLLNFPYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 200
 DB 121 VFIFPPSDEQLKSGTASVCLLNFPYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 180
 QY 201 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
 DB 181 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220
 RESULT 15
 ADK52334
 ID ADK52334 standard; protein; 220 AA.
 XX
 AC ADK52334;
 AC
 XX 20-MAY-2004 (first entry)
 DT
 XX Human anti-MCP-1 variable region light chain #10.
 DE
 XX monocyte chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;
 KW Antirheumatic; Nephrotropic; Antiartherosclerotic; Antipsoriatic;
 KW Vasotrophic; Immunosuppressive; Neuroprotective; Neoplastic;
 KW inflammatory condition; cancer; arthritis; multiple sclerosis;
 KW anti-MCP-1; heavy chain; light chain.
 XX

OS Homo sapiens.
XX WO2004016769-A2.
XX 26-FEB-2004.
XX 19-AUG-2003; 2003WO-US026232.
XX 19-AUG-2002; 2002US-0404802P.
XX (ABGE-) AGENIX INC.
XX Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;
XX Bhakta S;
XX WPI: 2004-203794/19.
XX N-PSDB; ADK52333.
XX New human monoclonal antibody that binds to monocyte chemo-attractant
PT protein-1 and is immobilized on an insoluble matrix, useful for
PT diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,
PT rheumatoid arthritis or psoriasis.
XX Claim 2; SEQ ID NO 40; 154pp; English.
XX The present invention relates to a human monoclonal antibody that binds
CC to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful
CC for the preparation of a medicament useful for treating neoplastic or
CC inflammatory conditions. The neoplastic disease is selected from breast
CC cancer, ovarian cancer, bladder cancer, lung cancer, colon cancer,
CC stomach cancer, endometrial cancer, kidney cancer, glioblastoma,
CC pancreatic cancer or prostate cancer. The inflammatory condition is
CC selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,
CC psoriasis, restenosis, autoimmune disease or multiple sclerosis. The
CC antibodies are also useful for diagnosing the above diseases. It is also
CC useful for the determining the level of MCP-1 and MCP-1 family members in
CC patient samples. The present sequence represents a human anti-MCP-1
CC variable region light chain sequence.
XX Sequence 220 AA;
SQ
Query Match 85.5%; Score 1063; DB 8; Length 220;
Best Local Similarity 91.8%; Pred. No. 2.2e-56;
Matches 202; Conservative 8; Mismatches 10; Indels 0; Gaps 0;
Qy 21 DIVMSQSPDSLAVSLGERVTINCKSSQSLLYSGNKNVLAWYQKPGSPKLLIYWASAR 80
Db 1 DIVMTQSPDSLAVSLGERATINCKSSQSLVYSSNNKNVLAWYQKPGPPKLLIYWASTR 60
Qy 81 ESGVDFRFGSGSGTDFLTITSSVQAEADVAVYQYQYYSYPLTFAGTKLEKETVAAPS 140
Db 61 ESGVDFRFGSGSGTDFLTITSSVQAEADVAVYQYQYYSYPLTFAGTKLEKETVAAPS 120
Qy 141 VFIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQSVTEQDSDSTYS 200
Db 121 VFIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQSVTEQDSDSTYS 180
Qy 201 LSSLTLSKADYKHKYKACVTHQGLSSPVTKSFNRGEC 240
Db 181 LSSLTLSKADYKHKYKACVTHQGLSSPVTKSFNRGEC 220

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OM protein - protein search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1136	91.4	240	4	US-09-301-593-36
3	1121.5	90.2	239	4	US-09-627-896B-22
4	1120.5	90.1	241	2	US-07-916-098A-56
5	1070	86.1	220	4	US-09-301-593-17
6	1064	85.6	220	3	US-08-952-235-1
7	1064	85.6	220	4	US-09-669-971-1
8	1019.5	82.0	239	3	US-08-812-586-29
9	1019.5	82.0	239	4	US-09-535-832A-30
10	994.5	80.0	235	4	US-09-472-087-14
11	994.5	80.0	235	4	US-09-472-087-65
12	991.5	79.8	233	4	US-09-472-087-15
13	991.5	79.8	233	4	US-09-472-087-67
14	987	79.4	236	4	US-09-859-053-34
15	985	79.2	234	4	US-09-472-087-17
16	985	79.2	234	4	US-09-472-087-69
17	977	78.6	236	4	US-09-859-053-38
18	974.5	78.4	239	4	US-10-000-489-8
19	969	78.0	234	3	US-09-049-672A-6
20	967	77.8	236	4	US-09-859-053-30
21	955.5	76.9	239	3	US-08-487-550-6
22	955.5	76.9	239	4	US-09-526-098-6
23	955.5	76.9	239	4	US-09-383-916-6
24	955	76.8	214	4	US-09-472-087-71
25	953	76.7	234	4	US-09-740-002-24
26	949	76.3	236	1	US-08-157-101A-5
27	944.5	76.0	235	3	US-09-171-945-97

28	941.5	75.7	232	1	US-08-704-744-80	Sequence 80, Appl
29	941.5	75.7	235	3	US-09-171-945-99	Sequence 99, Appl
30	941	75.7	218	2	US-08-887-352B-13	Sequence 13, Appl
31	941	75.7	218	3	US-08-466-151-9	Sequence 9, Appl
32	941	75.7	218	3	US-09-109-207C-13	Sequence 13, Appl
33	941	75.7	218	3	US-08-296-005-13	Sequence 13, Appl
34	941	75.7	218	3	US-08-466-163B-9	Sequence 9, Appl
35	941	75.7	218	4	US-09-920-171-13	Sequence 13, Appl
36	941	75.7	218	4	US-08-802-096-3	Sequence 9, Appl
37	941	75.7	218	4	US-09-802-077-9	Sequence 9, Appl
38	941	75.7	218	4	US-09-716-028-13	Sequence 13, Appl
39	941	75.7	218	4	US-10-113-996-13	Sequence 13, Appl
40	941	75.7	218	5	PCT-US96-13152-2	Sequence 2, Appl
41	940.5	75.7	235	3	US-09-171-945-52	Sequence 52, Appl
42	940	75.6	233	2	US-07-934-373C-25	Sequence 25, Appl
43	940	75.6	233	3	US-08-437-642B-25	Sequence 25, Appl
44	940	75.6	233	4	US-08-146-206C-25	Sequence 25, Appl
45	940	75.6	233	4	US-09-705-686-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1

US-09-301-593-28
; Sequence 28, Application US/09301593A
; Patent No. 6455677
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.189001
; CURRENT APPLICATION NUMBER: US/09/301.593A
; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086.049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-301-593-28

Query Match	93.8%	Score 1166;	DB 4;	Length 240;
Best Local Similarity	93.3%	Pred. No. 3.3e-88;		
Matches	224;	Conservative	9;	Mismatches 7; Indels 0; Gaps 0;
Qy	1	MDSQAQVLMILLVWSGTCGDIVMSQSPDSIAVSLGERVTLNCKSSQSLLYSGNQNYLA	60	
Db	1	MDSQAQVLMILLVWSGTCGDIVMSQSPDSIAVSLGERVTLNCKSSQSLLYSGNQNYLA	60	
Qy	61	WYQKQPGQSPKLLIYFASARESGVPDRFSGSGSGTDFTLTISQVAEDVAVYYCQYYSY	120	
Db	61	WFQKQPGQSPKLLIYFASARESGVPDRFSGSGSGTDFTLTISQVAEDVAVYYCQYYSY	120	
Qy	121	PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVIVCLNNFYPREAKVQWKNAL	180	
Db	121	PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVIVCLNNFYPREAKVQWKNAL	180	
Qy	181	QSGNSQESVTEQDSKDSYISLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC	240	
Db	181	QSGNSQESVTEQDSKDSYISLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC	240	

RESULT 2

US-09-301-593-36

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; Sequence 36, Application US/09301593A
; Patent No. 6455677
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.1890001
; CURRENT APPLICATION NUMBER: US/09/301.593A
; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086,049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 36
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-301-593-36
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Query Match 91.4%; Score 1136; DB 4; Length 240;
Best Local Similarity 90.0%; Pred. No. 9.6e-86;
Matches 216; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

Qy 1 MDSQAQVLMILLWVSGTCGDIVMSQSPDSLAIVSLGERVTINCKSSQSLLYSGNQKNYLA 60
Db 1 METDTLLWILLWVPGSGDIVMTQSPDSLAIVSLGERATINCKSSQSLLYSRNQKNYLA 60

Qy 61 WYQKPGQPKLLIYWASARESGVDPDRFSGSGGTDFLTITSSVQAEADVAVVYCOQYVS 120
Db 61 WYQKPGQPKLLIYFASARESGVDPDRFSGSGGTDFLTITSSVQAEADVAVVYCOQYVS 120

Qy 121 PLTEGAGTKLEKRTVAAPSVFPPSPDEQKSGTASVCLNNFYPREAKVQWKVDNAL 180
Db 121 PLTEGAGTKLEKRTVAAPSVFPPSPDEQKSGTASVCLNNFYPREAKVQWKVDNAL 180

Qy 181 QSGNSQSVTEQDSKDYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 240
Db 181 QSGNSQSVTEQDSKDYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 240
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```
RESULT 3
US-09-627-896B-22
; Sequence 22, Application US/09627896B
; Patent No. 6827934
; GENERAL INFORMATION:
; APPLICANT: CO, MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO
; APPLICANT: CARRENO, BEATRIZ CHERYL
; APPLICANT: CELNIKER, ABBIE CHERYL
; APPLICANT: COLLINS, MARY
; APPLICANT: GOLDMAN, SAMUEL
; APPLICANT: GRAY, GARY S.
; APPLICANT: KNIGHT, ANDREA
; APPLICANT: O'HARA, DENISE
; APPLICANT: RUP, BONITA
; APPLICANT: VELDMAN, GEERTRUIDA M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
; FILE REFERENCE: 08702.0081-01000
; CURRENT APPLICATION NUMBER: US/09/627.896B
; CURRENT FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 22
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Mus sp.
```

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; FEATURE:
; OTHER INFORMATION: 3d1 light chain
US-09-627-896B-22

Query Match 90.2%; Score 1121.5; DB 4; Length 239;
Best Local Similarity 90.4%; Pred. No. 1.5e-84;
Matches 217; Conservative 11; Mismatches 11; Indels 1; Gaps 1;

Qy 1 MDSQAQVLMILLWVSGTCGDIVMSQSPDSLAIVSLGERVTINCKSSQSLLYSGNQKNYLA 60
Db 1 MDSQAQVLMILLWVSGTCGDIVLTQSPDSLAIVSLGERATISCKSSQSLNSRTRENYLA 60

Qy 61 WYQKPGQPKLLIYWASARESGVDPDRFSGSGGTDFLTITSSVQAEADVAVVYCOQYVS 120
Db 61 WYQKPGQPKLLIYWASARESGVDPDRFSGSGGTDFLTITSSVQAEADVAVVYCOQYVS 120

Qy 121 PLTEGAGTKLEKRTVAAPSVFPPSPDEQKSGTASVCLNNFYPREAKVQWKVDNAL 180
Db 121 -YTFGQGTKEIKRTVAAPSVFPPSPDEQKSGTASVCLNNFYPREAKVQWKVDNAL 179

Qy 181 QSGNSQSVTEQDSKDYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 240
Db 180 QSGNSQSVTEQDSKDYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 239

RESULT 4
US-07-916-098A-56
; Sequence 56, Application US/07916098A
; Patent No. 5871732
; GENERAL INFORMATION:
; APPLICANT: BURKLY, LINDA C.
; APPLICANT: CHISHOLM, PATRICIA L.
; APPLICANT: THOMAS, DAVID W.
; APPLICANT: ROSA, MARGARET D.
; APPLICANT: ROSA, JOSEPH J.
; TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
; STREET: 10 SOUTH WACKER DRIVE
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: U.S.A.
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/916.098A
; FILING DATE: July 24, 1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/08843
; FILING DATE: No. 5871732ember 27, 1991
; CLASSIFICATION: 424
; APPLICATION NUMBER: 07/618,542
; FILING DATE: No. 5871732ember 27, 1990
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: JOHN J. MC DONNELL
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 92,310-G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 715-1000
; TELEX: 910/221-5317
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
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TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-916-098A-56

Query Match 90.1%; Score 1120.5; DB 2; Length 241;
Best Local Similarity 92.4%; Pred. No. 1.8e-84;
Matches 218; Conservative 6; Mismatches 11; Indels 1; Gaps 1;

Qy 5 AQLVLLLLWSGCTGDIWMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKYLAWYQQ 64
Db 7 AQLGLLLWLPFGARDIWTQSPDSLAVSLGERATINCKSSGSLLYSTNQKYLAWYQQ 66

Qy 65 KPGQPKLLIYWASAREGVPDRFSGSGGTDFTLTISVQAEADVAVYCOQYYSYPLTF 124
Db 67 KPGQPKLLIYWASTRESGVDRFSGSGGTDFTLTISLQAEADVAVYCOQYYSY-RTF 125

Qy 125 GAGTKLEKRTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN 184
Db 126 GRGTKLEIKRTVAAPSVFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN 185

Qy 185 SQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
Db 186 SQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 241

RESULT 5
US-09-301-593-17
; Sequence 17, Application US/09301593A
; Patent No. 6455677
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.1890001
; CURRENT APPLICATION NUMBER: US/09/301,593A
; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086,049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-301-593-17

Query Match 86.1%; Score 1070; DB 4; Length 220;
Best Local Similarity 93.2%; Pred. No. 2.3e-80;
Matches 205; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

Qy 21 DIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKYLAWYQKPGQSPKLLIYWASAR 80
Db 1 DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYSRNQKYLAWFQKPGQSPKLLIYWASTR 60

Qy 81 ESGVDPDRFSGSGGTDFTLTISVQAEADVAVYCOQYYSYPLTFGAGTKLEKRTVAAPS 140
Db 61 ESGVDPDRFTGSGFGDFDLTISVQAEADVAVYCOQYYSYPLTFGAGTKLEKRTVAAPS 120

Qy 141 VFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYS 200
Db 121 VFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYS 180

Qy 201 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
Db 181 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220

RESULT 6
US-08-952-235-1
; Sequence 1, Application US/08952235
; Patent No. 6207152
; GENERAL INFORMATION:
; APPLICANT: Schwall, Ralph H.
; APPLICANT: Tabor, Kelly H.
; TITLE OF INVENTION: Hepatocyte Growth Factor Receptor
; TITLE OF INVENTION: Antagonists and Uses Thereof
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/952,235
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/460368
; FILING DATE: 02-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P0938P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 220 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-952-235-1

Query Match 85.6%; Score 1064; DB 3; Length 220;
Best Local Similarity 90.9%; Pred. No. 7e-80;
Matches 200; Conservative 14; Mismatches 6; Indels 0; Gaps 0;

Qy 21 DIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKYLAWYQKPGQSPKLLIYWASAR 80
Db 1 DIVMSQSPSSLTVSVGEKVTVSCSSQSLLYTSQKYLAWYQKPGQSPKLLIYWASTR 60

Qy 81 ESGVDPDRFSGSGGTDFTLTISVQAEADVAVYCOQYYSYPLTFGAGTKLEKRTVAAPS 140
Db 61 ESGVDPDRFTGSGGTDFTLTITSVKADDLAVYCOQYVAYPWTGGGTGKLEIKRTVAAPS 120

Qy 141 VFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYS 200
Db 121 VFIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSTYS 180

Qy 201 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
Db 181 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220

RESULT 7
US-09-669-971-1
; Sequence 1, Application US/09669971
; Patent No. 6468529
; GENERAL INFORMATION:
; APPLICANT: Schwall, Ralph H.
; APPLICANT: Tabor, Kelly H.
; TITLE OF INVENTION: Hepatocyte Growth Factor Receptor
; Antagonists and Uses Thereof

;
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 1 DNA Way
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ;
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Winpatin (Genentech)
 ;
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/669,971
 ; FILING DATE: 05-Jul-2001
 ; CLASSIFICATION: <unknown>
 ;
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/952,235
 ; FILING DATE: <unknown>
 ; APPLICATION NUMBER: 08/460368
 ; FILING DATE: 02-JUN-1995
 ;
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Marschang, Diane L.
 ; REGISTRATION NUMBER: 35,600
 ; REFERENCE/DOCKET NUMBER: P0938P1
 ; TELEPHONE: 650/225-5416
 ; TELEFAX: 650/952-9881
 ;
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 220 amino acids
 ; TYPE: Amino Acid
 ; TOPOLOGY: Linear
 ;
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 ;
 ; US-09-669-971-1
 ;
 ; Query Match 85.6%; Score 1064; DB 4; Length 220;
 ; Best Local Similarity 90.9%; Pred. No. 7e-80;
 ; Matches 200; Conservative 14; Mismatches 6; Indels 0; Gaps 0;
 ;
 ; QY 21 DIVMSQSPDLSVSLGERVTLNCKSSQSLLYSGNKNLAWVQKPGOSPKLLIYASAR 80
 ; DB 1 DIMMSQSPSSLTVSVEKVTSCSSQSLLYTSSQKNYLAQKPGOSPKLLIYASTR 60
 ; QY 81 ESGVPDRFSGSGSGTDFTLTISVQAEDVAVVYCOQYYSYPLTFGAGTKLEKRTVAAPS 140
 ; DB 61 ESGVPDRFSGSGSGTDFTLTITSVKADDLAVVYCOQYAYPTFTGGTKLEKRTVAAPS 120
 ; QY 141 VFIPPSDEQLKSGTASVCLNNFYPREKQVQKVDNALQSGNSQESVTEQDSKSTYS 200
 ; DB 121 VFIPPSDEQLKSGTASVCLNNFYPREKQVQKVDNALQSGNSQESVTEQDSKSTYS 180
 ; QY 201 LSSLTLSKADYKHKYKACEVTHQGLSSPVTGKSNRGE 240
 ; DB 181 LSSLTLSKADYKHKYKACEVTHQGLSSPVTGKSNRGE 220
 ;
 ; RESULT 8
 ; US-08-812-586-29
 ; Sequence 29, Application US/08812586
 ; Patent No. 6048704
 ; GENERAL INFORMATION:
 ; APPLICANT: Martin David Tilson
 ; TITLE OF INVENTION: PURIFIED AND RECOMBINANT ANTIGENIC
 ; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH ABDOMINAL AORTIC ANEURYSM (AAA)
 ; TITLE OF INVENTION: DISEASE, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
 ; NUMBER OF SEQUENCES: 61
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cooper & Dunham LLP
 ; STREET: 1185 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York

;
 ; COUNTRY: U.S.A.
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/812,586
 ; FILING DATE: 07-MAR-1997
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: White, John P.
 ; REGISTRATION NUMBER: 28,678
 ; REFERENCE/DOCKET NUMBER: 0575/53862-A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 278-0400
 ; TELEFAX: (212) 391-0525
 ; INFORMATION FOR SEQ ID NO: 29:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 239 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-812-586-29
 ;
 ; Query Match 82.0%; Score 1019.5; DB 3; Length 239;
 ; Best Local Similarity 85.2%; Pred. No. 3.5e-76;
 ; Matches 201; Conservative 14; Mismatches 20; Indels 1; Gaps 1;
 ;
 ; QY 4 QAOVLMILLVWSGTCGDIVMSQSPDLSVSLGERVTLNCKSSQSLLYSGNKNYLAQY 63
 ; DB 4 QTVQFISLLWISG-AGDIVMTQSPDLSVSLGERATINCKSSQSLVYSSNNKNYLAQY 62
 ; QY 64 QKPGOSPKLLIYASARESGLVDFRFGSGSGSGTDFTLTISVQAEDVAVVYCOQYYSYPLT 123
 ; DB 63 QKPGQAPRLIYDASSRATGIPDRFGSGSGSGTDFTLTISRLEPDEFAVYGGQYGGSPLT 122
 ; QY 124 FGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVCLNNFYPREKQVQKVDNALQSG 183
 ; DB 123 FGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVCLNNFYPREKQVQKVDNALQSG 182
 ; QY 184 NSQESVTEQDSKSTYSLSSTLTLSKADYKHKYKACEVTHQGLSSPVTGKSNRGE 239
 ; DB 183 NSQESVTEQDSKSTYSLSSTLTLSKADYKHKYKACEVTHQGLSSPVTGKSNRGE 238
 ;
 ; RESULT 9
 ; US-09-535-832A-30
 ; Sequence 30, Application US/09535832A
 ; Patent No. 6537769
 ; GENERAL INFORMATION:
 ; APPLICANT: Tilson, Martin David
 ; TITLE OF INVENTION: Purified and Recombinant Antigenic Proteins Associated
 ; TITLE OF INVENTION: with Abdominal Aortic Aneurysm (AAA) Disease, and
 ; TITLE OF INVENTION: Diagnostic and Therapeutic use Thereof
 ; FILE REFERENCE: 53862-AZ
 ; CURRENT APPLICATION NUMBER: US/09/535,832A
 ; CURRENT FILING DATE: 2000-03-28
 ; NUMBER OF SEQ ID NOS: 57
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 30
 ; LENGTH: 239
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-535-832A-30
 ;
 ; Query Match 82.0%; Score 1019.5; DB 4; Length 239;
 ; Best Local Similarity 85.2%; Pred. No. 3.5e-76;
 ; Matches 201; Conservative 14; Mismatches 20; Indels 1; Gaps 1;
 ;
 ; QY 4 QAOVLMILLVWSGTCGDIVMSQSPDLSVSLGERVTLNCKSSQSLLYSGNKNYLAQY 63

Db 4 QTVFISLLWISG-AGIVMTQSPDLSLAVSLGERATINCKSSQSVLYSSNNKYLAWYQ 62
Qy 64 QKPGSPKLLIYWASARSGVDPDRFSGSGGTDFTLTISVQAEADVAVVYCOQYVSPLT 123
Db 63 QKPGQAPRLIYDASSRATGIPDRFSGSGGTDFTLTISRLPEPDAFVYVYQYGSPLT 122
Qy 124 FGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCILNNFYPREAKVQWKVDNALQSG 183
Db 123 FGGGKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCILNNFYPREAKVQWKVDNALQSG 182
Qy 184 NSQSVTEQDSKDSYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGE 239
Db 183 NSQSVTEQDSKDSYSLSSLTLSKADYKHKVYAGEVTHQGLSSPVTKSFNRGE 238

RESULT 10
US-09-472-087-14
; Sequence 14, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, BILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 14
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-14

Query Match 80.0%; Score 994.5; DB 4; Length 235;
Best Local Similarity 78.8%; Pred. No. 3.8e-74;
Matches 189; Conservative 27; Mismatches 19; Indels 5; Gaps 1;
Qy 1 MDSQAQVLMILLWVSGTCGDIWMSQSPDLSLAVSLGERVTLNCKSSQSLLYSGNQKNYLA 60
Db 1 METPAQLLFLILLWLPDPTTGEIVLTQSPGTLSLSPGERATLSRASQSI-----SSSFLA 55
Qy 61 WYQKPGSPKLLIYWASARSGVDPDRFSGSGGTDFTLTISVQAEADVAVVYCOQYVS 120
Db 56 WYQRPQAPRLIYGASSRATGIPDRFSGSGGTDFTLTISRLPEPDAFVYVYCOQYGS 115
Qy 121 PLTGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCILNNFYPREAKVQWKVDNAL 180
Db 116 PWTGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCILNNFYPREAKVQWKVDNAL 175
Qy 181 QSGNSQSVTEQDSKDSYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
Db 176 QSGNSQSVTEQDSKDSYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 235

RESULT 11
US-09-472-087-65
; Sequence 65, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, BILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.

; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 65
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-65

Query Match 80.0%; Score 994.5; DB 4; Length 235;
Best Local Similarity 78.8%; Pred. No. 3.8e-74;
Matches 189; Conservative 27; Mismatches 19; Indels 5; Gaps 1;
Qy 1 MDSQAQVLMILLWVSGTCGDIWMSQSPDLSLAVSLGERVTLNCKSSQSLLYSGNQKNYLA 60
Db 1 METPAQLLFLILLWLPDPTTGEIVLTQSPGTLSLSPGERATLSRASQSI-----SSSFLA 55
Qy 61 WYQKPGSPKLLIYWASARSGVDPDRFSGSGGTDFTLTISVQAEADVAVVYCOQYVS 120
Db 56 WYQRPQAPRLIYGASSRATGIPDRFSGSGGTDFTLTISRLPEPDAFVYVYCOQYGS 115
Qy 121 PLTGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCILNNFYPREAKVQWKVDNAL 180
Db 116 PWTGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCILNNFYPREAKVQWKVDNAL 175
Qy 181 QSGNSQSVTEQDSKDSYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
Db 176 QSGNSQSVTEQDSKDSYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 235

RESULT 12
US-09-472-087-15
; Sequence 15, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, BILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 15
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-15

Query Match 79.8%; Score 991.5; DB 4; Length 233;
Best Local Similarity 79.2%; Pred. No. 6.7e-74;
Matches 190; Conservative 23; Mismatches 20; Indels 7; Gaps 1;
Qy 1 MDSQAQVLMILLWVSGTCGDIWMSQSPDLSLAVSLGERVTLNCKSSQSLLYSGNQKNYLA 60
Db 1 METPAQLLFLILLWLPDPTTGEIVLTQSPGTLSLSPGERATLSRTSVS-----SSYLA 53
Qy 61 WYQKPGSPKLLIYWASARSGVDPDRFSGSGGTDFTLTISVQAEADVAVVYCOQYVS 120

Db 54 WYQKPGQAPRLIYGAASRATGIPDRFSGSGGTDFLTISRLEPEDFAVYVCOQYGIS 113
QY 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNAL 180
Db 114 PFTFGGKTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNAL 173
QY 181 QSGNSQESVTEQDSKDSYSLSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 240
Db 174 QSGNSQESVTEQDSKDSYSLSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 233

RESULT 13

US-09-472-087-67
; Sequence 67, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 67
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-67

Query Match 79.8%; Score 991.5; DB 4; Length 233;
Best Local Similarity 79.2%; Pred. No. 6.7e-74;
Matches 190; Conservative 23; Mismatches 20; Indels 7; Gaps 1;
QY 1 MDSQAQVLMILLWVSGTCGDIVMSQSPDSLAVSLGERVTINCKSSQLLYSGNQKNYLA 60
Db 1 METPAQLLFLLLWLPDPTTGEIVLTQSPGTLSLSPGERATLSRLEPEDFAVYVCOQY 53
QY 61 WYQKPGQSPKLLIYWASARESGVDPDRFSGSGGTDFLTISRLEPEDFAVYVCOQYYS 120
Db 54 WYQKPGQAPRLIYGAASRATGIPDRFSGSGGTDFLTISRLEPEDFAVYVCOQYGIS 113
QY 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNAL 180
Db 114 PFTFGGKTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNAL 173
QY 181 QSGNSQESVTEQDSKDSYSLSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 240
Db 174 QSGNSQESVTEQDSKDSYSLSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 233

RESULT 14

US-09-859-053-34
; Sequence 34, Application US/09859053
; Patent No. 6803039
; GENERAL INFORMATION:
; APPLICANT: Tsuji, Takashi
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, No. 6803039suaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; FILE REFERENCE: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508

; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-053-34

Query Match 79.4%; Score 987; DB 4; Length 236;
Best Local Similarity 78.8%; Pred. No. 1.6e-73;
Matches 190; Conservative 27; Mismatches 18; Indels 6; Gaps 2;
QY 1 MDSQAQVLMILLWVSGTCGDIVMSQSPDSLAVSLGERVTINCKSSQLLYSGNQKNYLA 60
Db 1 METPAQLLFLLLWLPDPTTGEIVLTQSPGTLSLSPGERATLSRLEPEDFAVYVCOQY 55
QY 61 WYQKPGQSPKLLIYWASARESGVDPDRFSGSGGTDFLTISRLEPEDFAVYVCOQYYS 120
Db 56 WYQKPGQAPRLIYGAASRATGIPDRFSGSGGTDFLTISRLEPEDFAVYVCOQYGS 115
QY 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNA 179
Db 116 PMSFGGKTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNA 175
QY 180 LOSGNSQESVTEQDSKDSYSLSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGE 239
Db 176 LOSGNSQESVTEQDSKDSYSLSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGE 235
QY 240 C 240
Db 236 C 236

RESULT 15

US-09-472-087-17
; Sequence 17, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 17
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-17

Query Match 79.2%; Score 985; DB 4; Length 234;
Best Local Similarity 78.3%; Pred. No. 2.3e-73;
Matches 188; Conservative 25; Mismatches 21; Indels 6; Gaps 1;
QY 1 MDSQAQVLMILLWVSGTCGDIVMSQSPDSLAVSLGERVTINCKSSQLLYSGNQKNYLA 60
Db 1 METPAQLLFLLLWLPDPTTGEIVLTQSPGTLSLSPGERATLSRLEPEDFAVYVCOQY 54
QY 61 WYQKPGQSPKLLIYWASARESGVDPDRFSGSGGTDFLTISRLEPEDFAVYVCOQYYS 120
Db 55 WYQKPGQAPRLIYGVSSRATGIPDRFSGSGGTDFLTISRLEPEDFAVYVCOQYGIS 114

Qy	121	PLTFGAGTKLELKRVTAAAPSVFI	PPPSDEQLKSGTASVVCLNNFY	PREAKVQWKVDNAL	180
Db	115	PFTFGPGTKVDIKRVTAAAPSVFI	PPPSDEQLKSGTASVVCLNNFY	PREAKVQWKVDNAL	174
Qy	181	QSGNSQESVTEQDSKDSSTYLS	SLSTLTLSKADYKHKVYACEVTH	QGLSSPVTKSFNRGEC	240
Db	175	QSGNSQESVTEQDSKDSSTYLS	SLSTLTLSKADYKHKVYACEVTH	QGLSSPVTKSFNRGEC	234

Search completed: March 23, 2005, 18:35:51
Job time : 25.6465 secs

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61 WYOOKPGOSP KLLIYWASARESGVPDRFSGSGGTDEFTLTISSVQAEADVAVYYCOOYYS 120

Qy 61 WYQKPGQSPKLLIYWASARESGVDRFSGSGGTDFLTITSSVQAEADVAVVYCOQYYSY 120
 Db 61 WYQKPGQSPKLLIYWASARESGVDRFSGSGGTDFLTITSSVQAEADVAVVYCOQYYSY 120
 Qy 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNAL 180
 Db 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNAL 180
 Qy 181 QSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEHKHYKVVACVTHQGLSSPVTKSFNREGC 240
 Db 181 QSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEHKHYKVVACVTHQGLSSPVTKSFNREGC 240

RESULT 5
 US-09-799-514-8
 ; Sequence 8, Application US/09799514
 ; Patent No. US2002006220A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Young et al.
 ; TITLE OF INVENTION: Immunoglobulin Superfamily Polynucleotides, Polypeptides, and An
 ; FILE REFERENCE: PTO15P1
 ; CURRENT APPLICATION NUMBER: US/09/799,514
 ; CURRENT FILING DATE: 2001-03-07
 ; PRIOR APPLICATION NUMBER: PCT/US00/23662
 ; PRIOR FILING DATE: 2000-08-29
 ; PRIOR APPLICATION NUMBER: 60/152,248
 ; PRIOR FILING DATE: 1999-09-03
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 8
 ; LENGTH: 240
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; ORGANISM: Mus sp.
 US-09-799-514-8

Query Match 90.5%; Score 1125; DB 9; Length 240;
 Best Local Similarity 90.3%; Pred. No. 4.3e-62;
 Matches 214; Conservative 10; Mismatches 13; Indels 0; Gaps 0;
 Qy 4 QAQVLMILLWVSGTCGDIWMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKNYLA 63
 Db 4 QTQVFISLLWISGAYGDIWMTQSPDSLAVSLGERATINCKSSQTLVLYSSDNKKNYLA 63
 Qy 64 QKPGQSPKLLIYWASARESGVDRFSGSGGTDFLTITSSVQAEADVAVVYCOQYYSYPLT 123
 Db 64 QKPGQSPKLLIYWASARESGVDRFSGSGGTDFLTITSSVQAEADVAVVYCOQYYSYPLT 123
 Qy 124 FGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSG 183
 Db 124 FGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSG 183
 Qy 184 NSQSVTEQDSKDSSTYSLSSTLTLSKADYEHKHYKVVACVTHQGLSSPVTKSFNREGC 240
 Db 184 NSQSVTEQDSKDSSTYSLSSTLTLSKADYEHKHYKVVACVTHQGLSSPVTKSFNREGC 240

RESULT 6
 US-10-630-406-8
 ; Sequence 8, Application US/10630406
 ; Publication No. US20040105855A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jure-Kunkel, Maria
 ; APPLICANT: Ganguly, Subinay
 ; APPLICANT: Abraham, Ralph
 ; APPLICANT: Hollenbaugh, Diane L.
 ; APPLICANT: Rillema, Jill
 ; APPLICANT: Thorne, Barbara
 ; APPLICANT: Shuford, Walter W.
 ; APPLICANT: Mittler, Robert S.
 ; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN 4-1BB
 ; FILE REFERENCE: D0288 NP
 ; CURRENT APPLICATION NUMBER: US/10/630,406

; CURRENT FILING DATE: 2003-07-30
 ; PRIOR APPLICATION NUMBER: US 60/399,646
 ; PRIOR FILING DATE: 2002-07-30
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 8
 ; LENGTH: 240
 ; TYPE: PRT
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic
 US-10-630-406-8

Query Match 90.3%; Score 1122; DB 16; Length 240;
 Best Local Similarity 90.0%; Pred. No. 6.6e-62;
 Matches 216; Conservative 10; Mismatches 14; Indels 0; Gaps 0;
 Qy 1 MDSQAQVLMILLWVSGTCGDIWMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKNYLA 60
 Db 1 MEPAQQLFLLLLWLPPTTGDIVMTQSPDSLAVSLGERATINCKSSQSLSSGNQKNYLA 60
 Qy 61 WYQKPGQSPKLLIYWASARESGVDRFSGSGGTDFLTITSSVQAEADVAVVYCOQYYSY 120
 Db 61 WYQKPGQSPKLLIYWASARESGVDRFSGSGGTDFLTITSSVQAEADVAVVYCOQYYSY 120
 Qy 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNAL 180
 Db 121 PLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNAL 180
 Qy 181 QSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEHKHYKVVACVTHQGLSSPVTKSFNREGC 240
 Db 181 QSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEHKHYKVVACVTHQGLSSPVTKSFNREGC 240

RESULT 7
 US-09-249-011A-22
 ; Sequence 22, Application US/09249011A
 ; Patent No. US20020176855A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CO, MAN SUNG
 ; APPLICANT: VASQUEZ, MAXIMILIANO
 ; APPLICANT: CARRENO, BEATRIZ
 ; APPLICANT: CELNIKER, ABBIE CHERYL
 ; APPLICANT: COLLINS, MARY
 ; APPLICANT: GOLDMAN, SAMUEL
 ; APPLICANT: GRAY, GARY S.
 ; APPLICANT: KNIGHT, ANDREA
 ; APPLICANT: O'HARA, DENISE
 ; APPLICANT: RUP, BONITA
 ; APPLICANT: VELDMAN, GEERTRUIDA M.
 ; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
 ; FILE REFERENCE: 08702.0081-00000
 ; CURRENT APPLICATION NUMBER: US/09/249,011A
 ; CURRENT FILING DATE: 1999-02-12
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 22
 ; LENGTH: 239
 ; TYPE: PRT
 ; ORGANISM: Mus sp.
 ; ORGANISM: Mus sp.
 US-09-249-011A-22

Query Match 90.2%; Score 1121.5; DB 9; Length 239;
 Best Local Similarity 90.4%; Pred. No. 7.1e-62;
 Matches 217; Conservative 11; Mismatches 11; Indels 1; Gaps 1;
 Qy 1 MDSQAQVLMILLWVSGTCGDIWMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKNYLA 60
 Db 1 MDSQAQVLMILLWVSGTCGDIWMTQSPDSLAVSLGERATINCKSSQSLSSGNQKNYLA 60
 Qy 61 WYQKPGQSPKLLIYWASARESGVDRFSGSGGTDFLTITSSVQAEADVAVVYCOQYYSY 120

Db 61 WYQKQPPKLLIYWASTRESGVDRFSGSGSGTDFLTITSSVQAEDVAVVYCSQSYNL 120
Qy 121 PLTGAGTKLEKRTVAAPSVFIIPPSDEQLKSGTASVCLNNFYPREAKVQKVDNAL 180
Db 121 -YTFGGTKVBIKRTVAAPSVFIIPPSDEQLKSGTASVCLNNFYPREAKVQKVDNAL 179
Qy 181 QSGNSQSVTQDSKDSYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNREGC 240
Db 180 QSGNSQSVTQDSKDSYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNREGC 239

RESULT 8
US-10-938-353-24
; Sequence 24, Application US/10938353
; Publication No. US20050059113A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: DEVALARAJA, MADHAV NARASIMHA
; APPLICANT: FOLTZ, IAN
; APPLICANT: HAAK-FREDSCHO, MARY
; APPLICANT: KELLERMANN, SIRID-ALMEE
; APPLICANT: LOW, JOSEPH EDWIN
; APPLICANT: MOBLEY, JAMES LESLIE
; TITLE OF INVENTION: ANTIBODIES TO M-CSF
; FILE REFERENCE: ABX-PP4
; CURRENT APPLICATION NUMBER: US/10/938,353
; PRIOR FILING DATE: 2004-09-09
; PRIOR APPLICATION NUMBER: 60/502,163
; PRIOR FILING DATE: 2003-09-10
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 24
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-938-353-24

Query Match 89.7%; Score 1115; DB 17; Length 240;
Best Local Similarity 89.5%; Pred. No. 1.8e-61;
Matches 212; Conservative 10; Mismatches 15; Indels 0; Gaps 0;
Qy 4 QAOVLMILLVWGTCGDIWMSQSPDSLAVSLGERVTNCKSSQSLLYSGNKNYLAWYQ 63
Db 4 QTVFISULLMISGADIVMTQSPDSLAVSLGERATINCKSSQSLIFSNKNYLAWYR 63
Qy 64 QKPGQPKLLIYWASARESGVDRFSGSGSGTDFLTITSSVQAEDVAVVYCOQYYSPLT 123
Db 64 QKPGQPNLLIYWASTRESGVDRFSGSGSGTDFLTITSSVQAEDVAVVYCOQYYSPT 123
Qy 124 FGAGTKLEKRTVAAPSVFIIPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSG 183
Db 124 FGQGTKEIKRTVAAPSVFIIPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSG 183
Qy 184 NSQSVTQDSKDSYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNREGC 240
Db 184 NSQSVTQDSKDSYSLSSLTLSKADYKHKVYACEVTHQGLSSPVTKSFNREGC 240

RESULT 9
US-10-644-277-20
; Sequence 20, Application US/10644277
; Publication No. US20050058639A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean M.
; APPLICANT: Haak-Frendscho, Mary
; APPLICANT: Poord, Orit
; APPLICANT: Liang, Meina L.
; APPLICANT: Ahluwalia, Kiran
; APPLICANT: Bhakta, Sunil
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO MONOCYTE
; FILE REFERENCE: CHEMO-ATTRACTANT PROTEIN-1 (MCP-1) AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/10/644,277

; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: 60/404,802
; PRIOR FILING DATE: 2002-08-19
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homosapien
US-10-644-277-20

Query Match 87.0%; Score 1082; DB 17; Length 220;
Best Local Similarity 93.6%; Pred. No. 1.8e-59;
Matches 206; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
Qy 21 DIVMSQSPDSLAVSLGERVTNCKSSQSLLYSGNKNYLAWYQKPGQSPKLLIYWASAR 80
Db 1 DIVMSQSPDSLAVSLGERATINCKSSQSLVYSSNNKNYLVWYQKPGQSPKLLIYWASIR 60
Qy 81 ESGVDRFSGSGSGTDFLTITSSVQAEDVAVVYCOQYYSVPLTFGAGTKLEKRTVAAPS 140
Db 61 ESGVDRFSGSGSGTDFLTITSSVQAEDVAVVYCOQYYSVPLTFGAGTKVEIKRTVAAPS 120
Qy 141 VFIFPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQSVTQDSKDSYTS 200
Db 121 VFIFPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQSVTQDSKDSYTS 180
Qy 201 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNREGC 240
Db 181 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNREGC 220

RESULT 10
US-09-301-593-17
; Sequence 17, Application US/09301593A
; Publication No. US20020052480A1
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.1890001
; CURRENT APPLICATION NUMBER: US/09/301,593A
; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086,049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-301-593-17

Query Match 86.1%; Score 1070; DB 9; Length 220;
Best Local Similarity 93.2%; Pred. No. 9.9e-59;
Matches 205; Conservative 9; Mismatches 6; Indels 0; Gaps 0;
Qy 21 DIVMSQSPDSLAVSLGERVTNCKSSQSLLYSGNKNYLAWYQKPGQSPKLLIYWASAR 80
Db 1 DIVMSQSPSSLAVSVEKVTMCSKSSQSLLYSRNQKNYLAWFQKPGQSPKLLIFWASTR 60
Qy 81 ESGVDRFSGSGSGTDFLTITSSVQAEDVAVVYCOQYYSVPLTFGAGTKLEKRTVAAPS 140
Db 61 ESGVDRFSGSGTDFLTITSSVQAEDVAVVYCOQYYSVPLTFGAGTKLEKRTVAAPS 120
Qy 141 VFIFPPSDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQSVTQDSKDSYTS 200

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Db 121 VFIFPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 180
Qy 201 LSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 240
Db 181 LSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 220

RESULT 11
US-10-159-006-17
; Sequence 17, Application US/10159006
; Publication No. US20030143229A1
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saidanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: FAPA-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.1890002
; CURRENT APPLICATION NUMBER: US/10/159,006
; CURRENT FILING DATE: 2002-08-03
; PRIOR APPLICATION NUMBER: US 09/301,593
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: EP 98107925.4
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: US 60/086,049
; PRIOR FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-159-006-17

Query Match 86.1%; Score 1070; DB 14; Length 220;
Best Local Similarity 93.2%; Pred. No. 9.9e-59;
Matches 205; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

Qy 21 DIVMSQSPDSLAVSLGERVTNLCKSSQSLLYSGNQKNYLAWYQKPGQSPKLLIYWASAR 80
Db 1 DIVMSQSPSSLTVSGEKVTVSCSKSSQSLLYSRNQKNYLAWYQKPGQSPKLLIFWASTR 60

Qy 81 ESGVPDRFSGSGGTDFLTITSSVQAEDVAVYCCQYYSYPLTFGAGTKLEKRTVAAPS 140
Db 61 ESGVPDRFTGSGFGTDFLTITSSVQAEDLAVYDCQYYSYPLTFGAGTKLEKRTVAAPS 120

Qy 141 VFIFPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 200
Db 121 VFIFPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 180

Qy 201 LSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 240
Db 181 LSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 220

RESULT 12
US-09-995-693-1
; Sequence 1, Application US/09995693
; Patent No. US20020136721A1
; GENERAL INFORMATION:
; APPLICANT: Schwall, Ralph H.
; APPLICANT: Tabor, Kelly H.
; TITLE OF INVENTION: Hepatocyte Growth Factor Receptor
; Antagonists and Uses Thereof
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA

Db 121 VFIFPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 180
Qy 201 LSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 240
Db 181 LSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 220
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; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/995,693
; FILING DATE: 29-No. US20020136721A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/952,235
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P0938P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 220 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-995-693-1

Query Match 85.6%; Score 1064; DB 9; Length 220;
Best Local Similarity 90.9%; Pred. No. 2.3e-58;
Matches 200; Conservative 14; Mismatches 6; Indels 0; Gaps 0;

Qy 21 DIVMSQSPDSLAVSLGERVTNLCKSSQSLLYSGNQKNYLAWYQKPGQSPKLLIYWASAR 80
Db 1 DIVMSQSPSSLTVSGEKVTVSCSKSSQSLLYTSSQKNYLAWYQKPGQSPKLLIYWASTR 60

Qy 81 ESGVPDRFSGSGGTDFLTITSSVQAEDVAVYCCQYYSYPLTFGAGTKLEKRTVAAPS 140
Db 61 ESGVPDRFTGSGGTDFLTITSSVKAEDLAVYCCQYYSYPLTFGAGTKLEKRTVAAPS 120

Qy 141 VFIFPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 200
Db 121 VFIFPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 180

Qy 201 LSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 240
Db 181 LSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 220

RESULT 13
US-10-232-408-1
; Sequence 1, Application US/10232408
; Publication No. US20030118587A1
; GENERAL INFORMATION:
; APPLICANT: Schwall, Ralph H.
; APPLICANT: Tabor, Kelly H.
; TITLE OF INVENTION: Hepatocyte Growth Factor Receptor
; Antagonists and Uses Thereof
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/232,408
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; FILING DATE: 03-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/669,971
; FILING DATE: 05-Jul-2001
; APPLICATION NUMBER: US/08/952,235
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/460368
; FILING DATE: 02-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P0938P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 220 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-232-408-1

Query Match      85.6%; Score 1064; DB 14; Length 220;
Best Local Similarity 90.9%; Pred. No. 2.3e-58;
Matches 200; Conservative 14; Mismatches 6; Indels 0; Gaps 0;

QY 21 DIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNKNYLAQYQKPGQSPKLLIYWASAR 80
DB 1 DIMSQSPSSLTYSVGEKVTYSCSSQSLLYTSQKNYLAQYQKPGQSPKLLIYWASTR 60
QY 81 ESGVPRDFSGSGGDTFTLTSSVQAEADVAVVYCOQYYSYPLTFGAGTKLEKRTVAAPS 140
DB 61 ESGVPRDFSGSGGDTFTLTSSVQAEADVAVVYCOQYYSYPLTFGAGTKLEKRTVAAPS 120
QY 141 VFIFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYS 200
DB 121 VFIFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYS 180
QY 201 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
DB 181 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220

RESULT 15
US-10-644-277-40
; Sequence 40, Application US/10644277
; Publication No. US20050058639A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean M.
; APPLICANT: Haak-Frendscho, Mary
; APPLICANT: Foord, Orit
; APPLICANT: Liang, Meina L.
; APPLICANT: Ahluwalia, Kiran
; APPLICANT: Bhakta, Sunil
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO MONOCYTE
; FILE REFERENCE: ABGENIX.091A
; CURRENT FILING DATE: 2003-08-19
; PRIOR FILING DATE: 2002-08-19
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homosapien
US-10-644-277-40

Query Match      85.5%; Score 1063; DB 17; Length 220;
Best Local Similarity 91.8%; Pred. No. 2.7e-58;
Matches 202; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 21 DIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNKNYLAQYQKPGQSPKLLIYWASAR 80
DB 1 DIVMTQSPDSLAVSLGERATINCKSSQSLYSSNNKNYLVYQQRPGOPPKLLIYWASTR 60
QY 81 ESGVPRDFSGSGGDTFTLTSSVQAEADVAVVYCOQYYSYPLTFGAGTKLEKRTVAAPS 140
DB 61 ESGVPRDFSGSGGDTFTLTSSVQAEADVAVVYCOQYYSYPLTFGAGTKLEKRTVAAPS 120
QY 141 VFIFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYS 200
DB 121 VFIFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYS 180
QY 201 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
DB 181 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220

Search completed: March 23, 2005, 18:40:02
Job time : 75.9394 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2005, 18:12:06 ; Search time 22.2222 Seconds
(without alignments)
1039.141 Million cell updates/sec

Title: US-10-058-069-9
Perfect score: 1243
Sequence: 1 MDSQAQVLMILLVWSGTG.....EVTHQGLSSPVTKSFNRGEC 240

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	975	78.4	240	2 S06084	Ig kappa chain pre
2	972	78.2	216	2 J80241	Ig kappa chain Am3
3	936.5	75.3	215	2 J80242	Ig kappa chain NIG
4	926.5	74.5	215	2 J80244	Ig kappa chain NIG
5	894.5	72.0	215	2 A3746	Ig kappa chain V-I
6	887.5	71.4	215	2 J80243	Ig kappa chain NIG
7	833	67.0	220	2 A31790	Ig kappa chain V r
8	800	64.4	214	2 S68212	Ig kappa chain (Ma
9	757.5	60.9	225	2 S37484	Ig kappa chain - m
10	737	59.3	234	2 S14237	Ig kappa chain pre
11	728.5	58.6	219	2 S38865	Ig kappa chain - m
12	727.5	58.5	219	2 S20208	Ig kappa chain - m
13	727.5	58.5	230	2 S33161	Ig kappa chain - s
14	725.5	58.4	217	2 S42772	Ig kappa chain - s
15	724.5	58.3	219	2 PC4203	Ig kappa chain (mo
16	724	58.2	218	2 S68241	Ig kappa chain V r
17	722	58.1	218	2 J85810	monoclonal antibod
18	718.5	57.8	219	2 S16112	Ig kappa chain V r
19	718	57.8	234	2 S01320	Ig kappa chain pre
20	700.5	56.4	235	2 S25058	Ig kappa chain - m
21	696.5	56.0	225	2 J70029	Ig kappa chain pre
22	675	54.3	210	2 A56169	Ig kappa chain V r
23	662	53.3	145	2 PL0014	Ig kappa chain pre
24	633	50.9	178	2 PT0219	Ig kappa chain V-C
25	619	49.8	138	2 S26040	Ig kappa chain pre
26	614	49.4	134	2 PC1214	Ig kappa chain pre
27	613.5	49.4	197	2 S29593	Ig kappa chain (WM
28	595	47.9	135	2 S2059	JC-kappa protein -
29	585.5	47.1	238	2 A49633	Ig lambda-like cha

30	577.5	46.5	229	2 A20969	Ig kappa chain pre
31	576	46.3	134	2 S49531	anti-Sm antibody V
32	573.5	46.1	133	2 PS0023	Ig kappa chain pre
33	566	45.5	134	1 K4HU17	Ig kappa chain pre
34	565.5	45.5	133	1 K4HUJ1	Ig kappa chain pre
35	559	45.0	129	2 S40347	Ig kappa chain - h
36	554	44.6	135	2 S38807	Ig light chain V-J
37	549.5	44.2	138	2 A53261	Ig kappa chain pre
38	549	44.2	132	2 S46373	Ig kappa chain V-J
39	548	44.1	106	1 K3HU	Ig kappa chain C r
40	542	43.6	124	2 S40364	Ig kappa chain - h
41	540	43.4	113	2 A49260	antitumor monoclon
42	537	43.2	121	1 K4HU	Ig kappa chain pre
43	537	43.2	136	2 A49137	Ig kappa chain pre
44	533	42.9	120	2 G33932	Ig kappa chain pre
45	530.5	42.7	118	2 PT0356	Ig kappa chain V r

ALIGNMENTS

RESULT 1

S06084
Ig kappa chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C:Accession: S06084
R:Crowe, J.S.; Smith, M.A.; Cooper, H.J.
Nucleic Acids Res. 17, 7992, 1989
A:Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain cDNA
A:Reference number: S06084; MUID:90016888; PMID:2508067
A:Accession: S06084
A:Molecule type: mRNA
A:Residues: 1-240 <CRO>
A:Cross-references: EMBL:X16129; NID:G56457; PIDN:CAA34256.1; PID:G56458
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-240/Product: Ig kappa chain #status predicted <MAT>
F:153-222/Domain: immunoglobulin homology <IMM>

Query Match	78.4%	Score	975;	DB	2;	Length	240;
Best Local Similarity	76.2%	Pred. No.	1.6e-59;				
Matches	183;	Conservative	20;	Mismatches	37;	Indels	0;
Qy	1	MDSQAQVLMILLVWSGTG	DI	VMSQSPDS	LA	VSIGERVT	LNCKSSQSLLYSGNQNYLA 60
Db	1	MESQTQVLMILLVWSGTG	DI	VMSQSPDS	LA	VSIGERVT	LNCKSSQSLLYSGNQNYLA 60
Qy	61	WYQKPGQSPKLLIYWAS	RG	SPDRPS	GS	SGTDF	TLTISVQAEDVAVYCOQYYSY 120
Db	61	WYQKPGQSPKLLIYWAS	RG	SPDRPS	GS	SGTDF	TLTISVQAEDVAVYCOQYYSY 120
Qy	121	PLTGGAGTKLEKRTVA	AP	SFIPPS	DEQLK	SGTAS	VVCLNNFYPREAKVQWVDNAL 180
Db	121	PYTFGAGTKLEKRTVA	AP	SFIPPS	DEQLK	SGTAS	VVCLNNFYPREAKVQWVDNAL 180
Qy	181	QSGNSQSVTVQD	SK	STYLS	STLS	KADYK	HVYACEVTHQGLSSPYTKSFNRGEC 240
Db	181	RDGVLDSVTQD	SK	STYLS	STLS	KADYK	HVYACEVTHQGLSSPYTKSFNRGEC 240

RESULT 2

J80241
Ig kappa chain Am37 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: J80241
R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, I.
submitted to JIPID, November 1998
A:Description: Structure relationship of kappa type light chains with AL amyloidosis: Mul
A:Reference number: J80241
A:Accession: J80241

A:Molecule type: protein
A:Residues: 1-216 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-92/Domain: immunoglobulin homology <IMM>

Query Match 78.2%; Score 972; DB 2; Length 216;
Best Local Similarity 86.8%; Pred. No. 2.2e-59;
Matches 191; Conservative 11; Mismatches 14; Indels 4; Gaps 3;

Qy 21 DIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKNYLAWYQKPGQSPKLLIYWASAR 80
Db 1 DIVLTQSPDFLAVSLGERATLNCKSSQSVLY--NSKNFLAWYQKPGQ--PKLLI-WANVR 56
Qy 81 ESGVPDRFSGSGGTDFTLTISQVQAEDVAVYVYCOQYYSYPLTFGAGTKLEKRTVAAPS 140
Db 57 ESGVPDRFSGSGGTDFTLTISQVQAEDVAVYVYCOQYYSYPLTFGAGTKLEKRTVAAPS 116
Qy 141 VFIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 200
Db 117 VFIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 176
Qy 201 LSSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
Db 177 LSSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 216

RESULT 3
JE0242
Ig kappa chain NIG26 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0242
R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T.
submitted to JTPID, November 1998
A:Description: Structure relationship of kappatype light chains with AL amyloidosis: Mul
A:Reference number: JE0241
A:Accession: JE0242
A:Molecule type: protein
A:Residues: 1-215 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 75.3%; Score 936.5; DB 2; Length 215;
Best Local Similarity 81.8%; Pred. No. 5.8e-57;
Matches 180; Conservative 18; Mismatches 17; Indels 5; Gaps 1;

Qy 21 DIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKNYLAWYQKPGQSPKLLIYWASAR 80
Db 1 EIVLTQSPGTLISLSPGERATLSCRASQSV-----SNNYLAWYQKPGQAPSLIYDASSR 55
Qy 81 ESGVPDRFSGSGGTDFTLTISQVQAEDVAVYVYCOQYYSYPLTFGAGTKLEKRTVAAPS 140
Db 56 ATGIPDRFSGSGGTDFTLTISGLEPEDFAVYVYCOQYDRPPTWTFGGTKVEIKRTVAAPS 115
Qy 141 VFIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 200
Db 116 VFIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 175
Qy 201 LSSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
Db 176 LSSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 215

RESULT 4
JE0244
Ig kappa chain NIG2 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0244
R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; T.
submitted to JTPID, November 1998
A:Description: A new subgroup of k type light chains (VkV) identified in cases of AL amy
A:Reference number: JE0243

A:Accession: JE0244
A:Molecule type: protein
A:Residues: 1-215 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 74.5%; Score 926.5; DB 2; Length 215;
Best Local Similarity 81.0%; Pred. No. 2.8e-56;
Matches 179; Conservative 22; Mismatches 13; Indels 7; Gaps 2;

Qy 21 DIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKNYLAWYQKPGQSPKLLIYWASAR 80
Db 1 EVLVTQSPATLISLSPGERATLSCRASQSV-----HSNLAWYQKPGQAPRLIYRASTR 54
Qy 81 ESGVPDRFSGSGGTDFTLTISQVQAEDVAVYVYCOQYYSY-PLTFGAGTKLEKRTVAAP 139
Db 55 ATGIPARFSGSGGTDFTLTISLQSEDFALYVYCOQYNTWPTPLTFGGGTKEIKRTVAAP 114
Qy 140 SVFIPPPDSQKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 199
Db 115 SVFIPPPDSQKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 174
Qy 200 LSSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
Db 175 LSSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 215

RESULT 5
A23746
Ig kappa chain V-III (KAU cold agglutinin) - human
C:Species: Homo sapiens (man)
C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C:Accession: A23746
R:Leoni, J.; Ghiso, J.; Frangione, B.
J. Biol. Chem. 266, 2836-2842, 1991
A:Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunogl
A:Reference number: A23746; MUID:91131575; PMID:1993660
A:Accession: A23746
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-215 <L80>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 72.0%; Score 894.5; DB 2; Length 215;
Best Local Similarity 81.3%; Pred. No. 4.2e-54;
Matches 178; Conservative 18; Mismatches 18; Indels 5; Gaps 1;

Qy 21 DIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKNYLAWYQKPGQSPKLLIYWASAR 80
Db 1 EIVLTQSPATLISLSPGERATLSCRASQSV-----SSNYLAWYQKPGQAPRLIYDASSR 55
Qy 81 ESGVPDRFSGSGGTDFTLTISQVQAEDVAVYVYCOQYYSYPLTFGAGTKLEKRTVAAPS 140
Db 56 ATGIPDRFSGSGGTDFTLTISLPLEPEDFAVYVYCOQYGGSSPLTFGGGTKEIKRTVAAPS 115
Qy 141 VFIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 200
Db 116 VFIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 175
Qy 201 LSSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGE 239
Db 176 LSSSTLTLSKADYKHKVYAGEVTHQGLSSPVTKSFNRGE 214

RESULT 6
JE0243
Ig kappa chain NIG93 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0243
R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; T.

submitted to JIPID, November 1998

A:Description: A new subgroup of k type light chains (Vkv) identified in cases of AL amy
A:Reference number: JE0243
A:Accession: JE0243
A:Molecule type: protein
A:Residues: 1-215 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>

```
Query Match      71.4%; Score 887.5; DB 2; Length 215;
Best Local Similarity 79.2%; Pred. No. 1.3e-53;
Matches 175; Conservative 20; Mismatches 19; Indels 7; Gaps 2;

QY 21 DIVMSQSPDSLAVSLGERVTNLCKSSQSLLYSGNKNYLAWYQKPGQSPKLLIYWASAR 80
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 EIVMTQSPATLSVSGERATISCRASQVATY-----VVWTKLQKQAPRLIYDASTR 54
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 81 ESGVDPDRFSGSGGTDFTLTISVQAEADVAVVYCOQYYSYPLTFGAGTKLEIK-RTVAAP 139
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 55 ATGVPAFSGSGGTEFTLTISLSQSEDFAIYYCQHNAWPPFTGGTKVETKRTVAAP 114
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 140 SVFIPTPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTY 199
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 115 SVFIPTPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTY 174
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 200 SLSSLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 240
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 175 SLSSLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 215
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

RESULT 7

QY 1790
Ig kappa chain V region (17/9) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
C:Accession: A31790
R:Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Scura, E.A.; Kenten, J.H.; Wilson, I.A.
J. Biol. Chem. 263, 17100-17105, 1988
A:Title: Preliminary crystallographic data, primary sequence, and binding data for an an
A:Reference number: A92686; MUID:89034213; PMID:3182835
A:Accession: A31790
A:Molecule type: mRNA
A:Residues: 1-220 <SCH>
A:Cross-references: GB:M23626; GB:J04061; NID:G533234; PIDN:AAA39162.1; PID:G533235
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

```
Query Match      67.0%; Score 833; DB 2; Length 220;
Best Local Similarity 70.9%; Pred. No. 6.6e-50;
Matches 156; Conservative 23; Mismatches 41; Indels 0; Gaps 0;

QY 21 DIVMSQSPDSLAVSLGERVTNLCKSSQSLLYSGNKNYLAWYQKPGQSPKLLIYWASAR 80
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 DIVMTQSPSSLTVTAGEKVTMSCTSSQSLFNSGKQKNYLTWYQKPGQPKVLIYWASTR 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 81 ESGVDPDRFSGSGGTDFTLTISVQAEADVAVVYCOQYYSYPLTFGAGTKLEIKRTVAAPS 140
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 ESGVDPDRFSGSGGTDFTLTISVQAEADVAVVYCOQYYSYPLTFGAGTKLEIKRADAAPT 120
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 141 VFIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYS 200
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 121 VSIFPPSEQLTSGGASVVCFLNNFYPKDINVKWIDGSRQNGVLNWTDOOSKSTYS 180
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 201 LSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 240
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 181 MSSTLTLSKADYERHNSYTCEATHKTSPIVKSFNREC 220
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

RESULT 8

QY 1790
Ig kappa chain (Mab03-1) - mouse (fragment)
C:Species: Mus musculus (house mouse)

C:Date: 29-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 11-Jan-2000
C:Accession: S68212
R:Tagaki, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
FEBS Lett. 375, 273-276, 1995
A:Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin
A:Reference number: S68211; MUID:96085223; PMID:7498516
A:Accession: S68212
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-214 <TAK>
A:Cross-references: EMBL:D29668
C:Superfamily: immunoglobulin V region; immunoglobulin homology

```
Query Match      64.4%; Score 800; DB 2; Length 214;
Best Local Similarity 70.1%; Pred. No. 1.1e-47;
Matches 150; Conservative 29; Mismatches 33; Indels 0; Gaps 0;

QY 21 DIVMSQSPDSLAVSLGERVTNLCKSSQSLLYSGNKNYLAWYQKPGQSPKLLIYWASAR 80
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 DIVMTQSPSSLTAMSVGQKVTMSCKSSQSLNSRQKNYLAQKPGQSPKLLVYFASTR 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 81 ESGVDPDRFSGSGGTDFTLTISVQAEADVAVVYCOQYYSYPLTFGAGTKLEIKRTVAAPS 140
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 ESGVDPDRFSGSGGTDFTLTISVQAEADVAVVYCOQYYSYPLTFGAGTKLEIKRADAAPT 120
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 141 VFIPPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYS 200
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 121 VSIFPPSEQLTSGGASVVCFLNNFYPKDINVKWIDGSRQNGVLNWTDOOSKSTYS 180
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 201 LSSTLTLSKADYERKHVYACEVTHQGLSSPVTKS 234
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 181 MSSTLTLSKADYERHNSYTCEATHKTSPIVKS 214
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

RESULT 9

QY 1790
Ig kappa chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000
C:Accession: S37484
R:Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A:Reference number: S37483
A:Accession: S37484
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-225 <DUC>
A:Cross-references: EMBL:X70424; NID:G406254; PIDN:CAA49869.1; PID:G406255
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

```
Query Match      60.9%; Score 757.5; DB 2; Length 225;
Best Local Similarity 63.4%; Pred. No. 9.3e-45;
Matches 147; Conservative 32; Mismatches 46; Indels 7; Gaps 2;

QY 9 MLLLIWVSGTCDIVMSQSPDSLAVSLGERVTNLCKSSQSLLYSGNKNYLAWYQKPGQ 68
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 VFLLLCVSGAGHSIVMTQPKLLLSAGDVTITCKASQSV-----SNDVAVYQKPGQ 54
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 69 SPKLLIYWASARESGVDPDRFSGSGGTDFTLTISVQAEADVAVVYCOQYYSYPLTFGAGT 128
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 55 SPKLLIYASRYTGVDPDRFTGSGVGTDTFTISTVQAEADVAVYCOQYYS-SYTFGGGT 113
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 129 KLEIKRTVAAPSVFIPTPPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQES 188
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 114 KLEIKRADAAPTIVSIPTPPSSQLTSGGASVVCFLNNFYPKDINVKWIDGSRQNGVLN 173
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 189 VTEQDSKSTYSLSSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 240
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 174 WTDQDSKSTYSMSSTLTLSKADYERHNSYTCEATHKTSPIVKSFNREC 225
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

RESULT 10

S14237
Ig kappa chain precursor (15C5) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S14237
R;Vandamme, A.M.; Bulens, F.; Bernar, H.; Nelles, L.; Lijnen, R.H.; Collen, D.
Eur. J. Biochem. 192, 767-775, 1990
A;Title: Construction and characterization of a recombinant murine monoclonal antibody
A;Reference number: S14236; MUID:9106173; PMID:2209622
A;Accession: S14237
A;Molecule type: mRNA
A;Residues: 1-234 <VAN>
A;Cross-references: EMBL:X56394; NID:951622; PIDN:CAA39805.1; PID:951623
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>

Query Match 59.3%; Score 737; DB 2; Length 234;
Best Local Similarity 58.8%; Pred. No. 2.4e-43;
Matches 141; Conservative 35; Mismatches 58; Indels 6; Gaps 1;

QY 1 MDQAOAVMLLLWVGSTCGDIIVMQSQPSDSLAVSLGERVTLNCKSQSLIYSGNQKNYLA 60
DB 1 MRPAPFLGILLWFPQIKDIIKNTQSPSWYASLGERVTVCASQDI-----NSYLS 54
QY 61 WYQKPGQSPKLIYWASARESPVPRFSGSGSGTFTLTITSSVQAEDVAVYVCOQYYS 120
DB 55 WIQKPGKSPKLIYRGNRLVAGVPSPFSGSGSGQDYSLTISSEYEDVGVIYCLAYDEF 114
QY 121 PLTFGAGTKLELKRVTVAAPSVFTPPSPDEQLKSGTASVCLLNFPYPREAKVQWKVDNAL 180
DB 115 PFTFGSGTKLEIKRAAAPTVSIFPPSPSEQLTSGGASVVCFLNFPYKPDINVKWKIDGSE 174
QY 181 QSGNSQESVTEQDSKSTYSLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
DB 175 RQGVLSNWTDDQDSKSTYSMSSTLTITKDEYRHSNYTCEATHTKSTSPVKSFNREC 234

RESULT 11
S38865
Ig kappa chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 15-Jun-2001
C;Accession: S38865
R;Kipp, B.; Becker, W.; Schlaak, M.
submitted to the EMBL Data Library, November 1993
A;Description: Combination of a defined specificity and desired isotype by cloning of an
A;Reference number: S38864
A;Accession: S38865
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-219 <KIP>
A;Cross-references: EMBL:Z27396; NID:9416538; PIDN:CAA81787.1; PID:9416539
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 58.6%; Score 728.5; DB 2; Length 219;
Best Local Similarity 63.2%; Pred. No. 8.5e-43;
Matches 139; Conservative 32; Mismatches 48; Indels 1; Gaps 1;

QY 21 DIVMQSQPSDSLAVSLGERVTLNCKSQSLIYSGNQKNYLAWYQKPGQSPKLIYWASAR 80
DB 1 ELVWTSPLSVSLGDOASISCRSQSLVHT-NGNTYLHWYLOKPLSLIYIVSNR 59
QY 81 ESGVPRFSGSGSGTFTLTITSSVQAEDVAVYVCOQYYSYPLTFGAGTKLELKRVTVAAPS 140
DB 60 FSGVPRFSGSGSGTFTLTISRVEADLVGYFCSQVTHVPWTFGGGTKEIKRAAAPT 119
QY 141 VFIFPPSPDEQLKSGTASVCLLNFPYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYS 200
DB 120 VSIFFPSSEQLTSGGASVVCFLNFPYKPDINVKWKIDGSRQGVLSNWTDDQDSKSTYS 179
QY 201 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240

```

Db      :|||||:|:|:|:| |||||:|:|:|:|:|:|:|:|:|:|:|:|:|
180 MSSTLTITKDEYERHNSYTCEATHKTSTSPIVKSFNRGEC 219


RESULT 12
S52028
Ig kappa chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S52028
R;van Engelen, F.; Schouten, A.; Molthoff, J.W.; Roosien, J.; Dirkee, W.G.; Schots, A.;
submitted to the EMBL Data Library, August 1994
A;Description: Coordinate expression of antibody subunit genes yields high levels of fun
A;Reference number: S52028
A;Accession: S52028
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-219 <VAN>
A;Cross-references: EMBL:L35138; NID:g522336; PIDN:AAA67525.1; PID:g522337
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match          58.5%; Score 727.5; DB 2; Length 219;
Best Local Similarity 63.6%; Pred. No. 9.9e-43;
Matches 140; Conservative 29; Mismatches 50; Indels 1; Gaps 1;

QY    21 DIVMSQPSDLSVLGERTLVLNCKSSQSLLYSGNQKNYLAWYQOKPGQSPKLLIYWASAR 80
DB    1 DVVTMSGPLSLPVSLGQAISICRSSQSIVHS-NNGTYLEWLQRPQGSPKLLIYKVSNR 59

QY    81 ESGVPDRFGSGSGTDFTLTISSVQAEADVAVYYCOQYYSYPLTFAGTGLELKRTVAAPS 140
DB    60 FSGVPDRFGSGSGTDFTLKISRVEADLGYYCYCFQGSHPPTFFGGTNLEIKRADAPT 119

QY    141 VFIPPSDELQKSGTASVVCLLNFPYREAKVQWKVDNALQSGNSQESVTEQDSKDYSTS 200
DB    120 VSIFPPSEQLTSGCASCVVCLNNFPYPKDINKWKIDGSRQGVNLNSWTDDQSKDYSTS 179

QY    201 LSSTLTILSKADYEKHVKYACETHVHQGLSSPVTKSFNRGEC 240
DB    180 MSSTLTITKDEYERHNSYTCEATHKTSTSPIVKSFNRGEC 219


RESULT 13
S33161
Ig kappa chain - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
C;Accession: S33161
R;Foley, R.C.; Beh, K.J.
submitted to the EMBL Data Library, July 1990
A;Description: Isolation and characterisation of sheep kappa light chain cDNA.
A;Reference number: S33161
A;Accession: S33161
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-230 <FO>
A;Cross-references: EMBL:X54110; NID:g297103; PIDN:CAA38046.1; PID:g1364221
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;143-212/Domain: immunoglobulin homology <IMM>

Query Match          58.5%; Score 727.5; DB 2; Length 230;
Best Local Similarity 58.9%; Pred. No. 1e-42;
Matches 139; Conservative 40; Mismatches 50; Indels 7; Gaps 2;

QY     6 QVLMLLLIW-VSGTCGDIVMSQPSDSLAVSLGERVTLNCKSSQSLLYSGNQKNYLAWYQQ 64
DB    1 QLGLGLLLWLPGARCDIQVTSQSSLSASTERVISICTRSQSV-----SNLYLWYQQ 54

QY    65 KPQSQPKLLIYWASRESGVDPFRFGSGSGTGDTFLTIISSVQAEADVAVYYCOQYYSPLTF 124

```

Db 55 KPGQAPKLLIYYATRLHTDVPFRFSGSGGTDYTLTISNLEANDTATYCYQVESTPLAF 114
Qy 125 GACTKLELKRVAAPSPVIFPPSPDEQLKSGTASVUCLLNPNYPREAKVQKVDNALQSGN 184
Db 115 GGGTNEIKRDAQPSVFLFKPSEQLRTGTGVVUCLVNDPYPKDINVKKVQVDGVTQNSN 174
Qy 185 SQESVTEQDSKDYSLSSSTLTLSKADYKHKVACEVTHQGLSSPVTKSFNRGEC 240
Db 175 FQNSFTDQDSKDYSLSSSTLTLSSEYQSHNAYACEVSHKSLPTALVKSFNRKNEC 230

RESULT 14

S42772
Ig kappa chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S42772
R:Schellekens, G.A.
submitted to the EMBL Data Library, November 1993
A:Reference number: S42771
A:Accession: S42772
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-217 <SCH>
A:Cross-references: EMBL:X75536; NID:G414143; PIDN:CAA53226.1; PID:G414144
C:Superfamily: immunoglobulin V region, immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:14-93/Domain: immunoglobulin homology <IMM>

Query Match 58.4%; Score 725.5; DB 2; Length 217;
Best Local Similarity 63.3%; Pred. No. 1.3e-42;
Matches 138; Conservative 31; Mismatches 48; Indels 1; Gaps 1;
Qy 23 VMSQSPDSLAVSLGERVTNLCKSSQSLLYSGNKNYLAWYQOKPGQSPKLLIYWASAR 82
Db 1 VMTQSPSLPVSGLDQASISCRSSQSLVHT-NGNTYLHWYLPKQSPKVLIVKVSRTFS 59
Qy 83 GVPDRFSGSGGTDFTLTISSVQAEADVAVYYCQYYSPYPLTFGAGTKLELKRVAAPSVF 142
Db 60 GVPDRFSGSGGTDFTFKISRVEADLGYYVCFQGSHPVPTFTGGGKLEIKRADAAAPTFS 119
Qy 143 IFPPSPDEQLKSGTASVUCLLNPNYPREAKVQKVDNALQSGNSQBSVTEQDSKDYSLSS 202
Db 120 IFPPSPDEQLKSGTASVUCLLNPNYPREAKVQKVDNALQSGNSQBSVTEQDSKDYSLSS 179
Qy 203 STLTLSKADYKHKVACEVTHQGLSSPVTKSFNRGEC 240
Db 180 STLTLSKADYKHKVACEVTHQGLSSPVTKSFNRGEC 217

RESULT 15

PC4203
Ig kappa chain (monoclonal antibody Maba34) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 11-Jan-2000
C:Accession: PC4203
R:Kwak, J.W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.; Park, Y.B.; Han, M.H.
Gene 173, 257-259, 1996
A:Title: Cloning and characterization of cDNAs coding for heavy and light chains of a monoclonal antibody Maba34
A:Reference number: PC4202; MUID:97082978; PMID:8964510
A:Accession: PC4203
A:Molecule type: mRNA
A:Residues: 1-219 <KWA>
A:Cross-references: GB:U29147; NID:G1594225; PIDN:AAC52821.1; PID:G1594226
C:Comment: This protein is specific for human plasma apolipoprotein A-I of high-density lipoprotein (HDL) particles.
C:Superfamily: immunoglobulin V region, immunoglobulin homology
F:1-112/Domain: V region #status predicted <VRG>
F:113-219/Domain: C region #status predicted <CRG>

Query Match 58.3%; Score 724.5; DB 2; Length 219;
Best Local Similarity 62.7%; Pred. No. 1.6e-42;
Matches 138; Conservative 32; Mismatches 49; Indels 1; Gaps 1;

Qy 21 DIVMSQSPDSLAVSLGERVTNLCKSSQSLLYSGNKNYLAWYQOKPGQSPKLLIYWASAR 80
Db 1 DVLMTQIPLSLPVSLGQASISCRSSQSLVHT-NGNTYLEWYLPKQSPKLLIYKVSNR 59
Qy 81 ESGVDPDRFSGSGGTDFTLTISSVQAEADVAVYYCQYYSPYPLTFGAGTKLELKRVAAPSV 140
Db 60 FSGVDPDRFSGSGGTDFTLTKISRVEADLGYYVCFQGSHPVPTFTGGGKLEIKRADAAAPT 119
Qy 141 VFIFPPSPDEQLKSGTASVUCLLNPNYPREAKVQKVDNALQSGNSQBSVTEQDSKDYSLSS 200
Db 120 VSIFPPSPSEQLTSGCASVWCFLNNFYPKDNVKKIDGSRQNGVLSNWTDDQDSKDYSLSS 179
Qy 201 LSSTLTLSKADYKHKVACEVTHQGLSSPVTKSFNRGEC 240
Db 180 MSSTLTLTLDKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 219

Search completed: March 23, 2005, 18:36:52
Job time : 23.2222 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 23, 2005, 18:05:41 ; Search time 92.5253 Seconds
(without alignment)
1328.275 Million cell updates/sec

Title: US-10-058-069-9
Perfect score: 1243
Sequence: 1 MDSQAQVLMLLLVSGTCG.....EVTHQGLSSPYTKSFNRGEC 240

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	998	80.3	240	Q6PIH6	Q6pih6 homo sapien
2	985.5	79.3	235	Q6GMV9	Q6gmv9 homo sapien
3	983.5	79.1	239	Q8NEK0	Q8nek0 homo sapien
4	983	79.1	236	Q6PIL8	Q6pil8 homo sapien
5	977.5	78.6	235	Q6GMW0	Q6gmw0 homo sapien
6	977.5	78.6	235	Q6PJP2	Q6pjf2 homo sapien
7	976.5	78.6	239	Q8TCD0	Q8tcd0 homo sapien
8	975	78.4	236	Q6P5S8	Q6p5s8 homo sapien
9	974	78.4	236	Q6GMX8	Q6gmx8 homo sapien
10	968	77.9	234	Q72473	Q72473 homo sapien
11	965	77.6	236	Q6GMW1	Q6gmw1 homo sapien
12	965	77.6	236	Q6GMX0	Q6gmx0 homo sapien
13	963	77.5	236	Q723Y4	Q723y4 homo sapien
14	959.5	77.2	239	Q6P491	Q6p491 homo sapien
15	958	77.1	236	Q6PIT5	Q6pit5 homo sapien
16	954	76.7	236	Q6PIH7	Q6pih7 homo sapien
17	953	76.7	236	Q6GMX9	Q6gmx9 homo sapien
18	935	75.2	236	Q6PIH4	Q6pih4 homo sapien
19	809	65.1	241	Q63ZX4	Q63zx4 mus musculus
20	767	61.7	238	Q66JS7	Q66js7 mus musculus
21	742	59.7	236	Q7TS98	Q7ts98 mus musculus
22	725.5	58.4	219	Q65ZC0	Q65zc0 mus musculus
23	630	50.7	237	Q7S236	Q7sz36 xenopus lae
24	617.5	49.7	243	Q6NTU5	Q6ntu5 xenopus lae
25	595	47.9	120	Q6P5R5	Q6p5r5 homo sapien
26	579	46.6	134	Q6V4C	Q6v4c HUMAN
27	565.5	45.5	133	Q6V4B	Q6v4b HUMAN
28	548	44.1	106	KAC	KAC HUMAN
29	537	43.2	121	Q6V4A	Q6v4a HUMAN
30	532	42.8	114	Q6V4A	Q6v4a HUMAN
31	493	39.7	255	Q6KB05	Q6kb05 mus musculus

32	479	38.5	109	1	KV4D_HUMAN
33	470	37.8	236	2	Q8NEJ1
34	464	37.3	236	2	Q6GMX4
35	460	37.0	236	2	Q6PIQ7
36	458	36.8	236	2	Q6IPQ0
37	456.5	36.7	235	2	Q6IN99
38	455.5	36.6	233	2	Q8TBC9
39	452.5	36.4	129	1	KV3L_HUMAN
40	449.5	36.2	129	1	KV3M_HUMAN
41	443	35.6	236	2	Q6GMX3
42	441.5	35.5	234	2	Q8N355
43	441.5	35.5	235	2	Q6PIK1
44	440.5	35.4	234	2	Q6GMW3
45	439.5	35.4	235	2	Q99M11

ALIGNMENTS

RESULT 1

ID	Q6PIH6	PRELIMINARY;	PRT;	240 AA.
AC	Q6PIH6;			
DT	05-JUL-2004	(TrEMBLrel. 27, Created)		
DT	05-JUL-2004	(TrEMBLrel. 27, Last sequence update)		
DT	05-JUL-2004	(TrEMBLrel. 27, Last annotation update)		
DE	Hypothetical protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lung;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,			
RA	Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzyszinski M.I., Skalska U., Smalusz D.B., Schnerch A., Schein J.E.,			
RA	Jones S.J., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RN	[2]			
RC	TISSUE=Lung;			
RA	Strausberg R.;			
RL	Submitted (JUL-2002) to the EMBL/GenBank/DBDJ databases.			
DR	EMBL; BC034142; AAH34142.1; -.			
DR	HSSP; P01837; 1KB5.			
DR	InterPro; IPR003599; IG.			
DR	InterPro; IPR007110; IG-like.			
DR	InterPro; IPR003597; IG cl.			
DR	InterPro; IPR003006; IG_MHC.			
DR	InterPro; IPR003596; IG_v.			
DR	Pfam; PF07654; Cl-set; 1.			
DR	SMART; SM00409; IG; 2.			
DR	SMART; SM00406; IGV; 1.			
DR	SMART; SM00835; IG LIKE; 2.			
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_1.			

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KW Hypothetical protein.
SQ SEQUENCE 240 AA; 26234 MW; 188D4DD8B8781EC4 CRC64;

  Query Match      80.3%; Score 998; DB 2; Length 240;
  Best Local Similarity 83.1%; Pred. No. 5.1e-75;
  Matches 197; Conservative 15; Mismatches 23; Indels 2; Gaps 2;

QY 5 AQLVLLMLLVSGTCDIVMSQSPDSLAVSLGERVTLNCKSSQSLLYSGNQKNYLAWYQQ 64
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 5 AQLGLLMLVSGSGDIVMAQSPLSVTPGPASISCRSSQSLHS-NGYNFYDWLQ 63

QY 65 KPGQPKLLIYWASARESGVDPDRFSGSGGTDFTLTISSVQAEADVAVYCOQYYSY 123
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 64 KPGQSPQLLIYWGNSRASGVPDRFSGSGGTDFTLKISRVEAEDGVYCYCMAQLQTPPYT 123

QY 124 FGAGTKLEKRTVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL 183
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 124 FQGQTKLEIKRTVAAPSVFIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL 183

QY 184 NSQSVTEQDSKSTYSLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 184 NSQSVTEQDSKSTYSLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240

RESULT 2
Q6GMV9 PRELIMINARY; PRT; 235 AA.
AC Q6GMV9;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickinson M.C.,
RA Blakesley R.W., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski A.C., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073793; AAH73793.1; --
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG.
DR InterPro; IPR003597; IG.
DR InterPro; IPR003006; IG.
DR InterPro; IPR003596; IG.
DR Pfam; PF07654; CI-set; 1.
DR Pfam; PF00047; IG; 2.
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DR PIR: S40342; S40342.
DR PIR: S40357; S40357.
DR HSP: P01834; 117Z.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig cl.
DR InterPro: IPR003006; Ig MHC.
DR InterPro: IPR003596; Ig v.
DR Pfam: PF07654; Cl-set; 1.
DR SMART: SM00406; IGv; 1.
DR PROSITE: PS0835; IG LIKE; 2.
DR PROSITE: PS00290; IG MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552C0A CRC64;

Query Match 79.1%; Score 983.5; DB 2; Length 239;
Best Local Similarity 81.8%; Pred. No. 8.3e-74;
Matches 193; Conservative 15; Mismatches 74; Indels 1; Gaps 1;

QY 5 AQLVLLMLLVSGTCDIVMSQSPDSLAVSLGERTVTLNCKSSQSLLYSGNQKNYLA 64
DB 5 AQLGLLMLVSGSGDVMQSPDLVPTGPEPASISCRSSQSLHSDGY-NYLDWYLQ 63

QY 65 KPGSPKLLIYWASARESGVDFRFGSGSGGTDFTLTISVQAEADVAVYCYQYYSPLTF 124
DB 64 KPGSPQLLIYLGNSRAGSGVDFRFGSGSGGTDFTLTISKVEAEDVGIIYCNQGLQTPQTF 123

QY 125 GAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN 184
DB 124 QGQIKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNTLQSGN 183

QY 185 SOESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRRGEC 240
DB 184 SOESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRRGEC 239

RESULT 4
Q6PIL8 PRELIMINARY; PRT; 236 AA.
ID Q6PIL8
AC Q6PIL8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywicki M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.

```

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RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC032451; AAH32451.1; -.
DR HSP: P01837; IKCU.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig cl.
DR InterPro: IPR003006; Ig MHC.
DR InterPro: IPR003596; Ig v.
DR Pfam: PF07654; Cl-set; 1.
DR SMART: SM00409; IG; 2.
DR SMART: SM00406; IGv; 1.
DR PROSITE: PS0835; IG LIKE; 2.
DR PROSITE: PS00290; IG MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25834 MW; 6647A9E77A3C0053 CRC64;

Query Match 79.1%; Score 983; DB 2; Length 236;
Best Local Similarity 78.4%; Pred. No. 8.9e-74;
Matches 189; Conservative 26; Mismatches 20; Indels 6; Gaps 2;

QY 1 MDSQAQVLMILLVWSGTCGDIVMSQSPDSLAVSLGERTVTLNCKSSQSLLYSGNQKNYLA 60
DB 1 METPAQLLFLLLWLPDSTGENVLTQSPGTLSPGERATLSCRASQSL-----SSSYLA 55

QY 61 WYQKPGSPKLLIYWASARESGVDFRFGSGSGGTDFTLTISVQAEADVAVYCYQYYS 119
DB 56 WYQKPGQAPRLIYGVSSRATGIPDRFGSGSGGTDFTLTISRLEPEDFAVYCYQYGT 115

QY 120 YPLTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA 179
DB 116 RPIITFGQTRLDIIRKTVAAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNA 175

QY 180 LOSGNSQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRRGEC 239
DB 176 LOSGNSQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRRGEC 235

QY 240 C 240
DB 236 C 236

RESULT 5
Q6GMW0 PRELIMINARY; PRT; 235 AA.
ID Q6GMW0
AC Q6GMW0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywicki M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.

```

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RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schmerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC073792; AAH73792.1; --
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR003596; IG v.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25765 MW; 4360C36B6D4133F5 CRC64;

Query Match 78.6%; Score 977.5; DB 2; Length 235;
Best Local Similarity 78.8%; Pred. No. 2.6e-73;
Matches 190; Conservative 26; Mismatches 18; Indels 7; Gaps 2;

Qy 1 MDSQAVMLLLWVSGTCGDIVMSQSPDSLAVSLGERVTNLCKSSQSLYSNGNKNYLA 60
Db 1 MEAPQALLFLLLWLPDSTGEIVMTQSPATLSVSPGERATLSCRASQI-----SNNLA 54

Qy 61 WYQKPGQSKLLIYWASRGVDPDRFGSGSGTDFTLTSSVQADVAVYCCQYYSY 120
Db 55 WYQRPQGPQRLIYGASSRVTGIPGRFSGSGSGTFTLSLSLQSEDFAVYFCQYNDW 114

Qy 121 PL-TFGAGTKLELKRVTVAAPSVFIPPPSDEQLKSGTASVCLNNFYPREAKVQKVDNA 179
Db 115 LLYFGQTKLELKRVTVAAPSVFIPPPSDEQLKSGTASVCLNNFYPREAKVQKVDNA 174

Qy 180 LQSGNSQSVTEQDSKSTYLSSTLTLSKADYEHKHYACEVTHQGLSSPVTKSNRGE 239
Db 175 LQSGNSQSVTEQDSKSTYLSSTLTLSKADYEHKHYACEVTHQGLSSPVTKSNRGE 234

Qy 240 C 240
Db 235 C 235

RESULT 6
Q6PJF2 PRELIMINARY; PRT; 235 AA.
ID Q6PJF2
AC Q6PJF2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haleh F.,

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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schmerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC016380; AAH16380.1; --
DR HSSP; P01837; 1KCU.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR003596; IG v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25520 MW; F33A145A396BA285 CRC64;

Query Match 78.6%; Score 977.5; DB 2; Length 235;
Best Local Similarity 77.9%; Pred. No. 2.6e-73;
Matches 187; Conservative 27; Mismatches 21; Indels 5; Gaps 1;

Qy 1 MDSQAVMLLLWVSGTCGDIVMSQSPDSLAVSLGERVTNLCKSSQSLYSNGNKNYLA 60
Db 1 METPAQLFLLLWLPDSTGEIVMTQSPATLSVSPGERATLSCRASQI-----SSAYLA 55

Qy 61 WYQKPGQSKLLIYWASRGVDPDRFGSGSGTDFTLTSSVQADVAVYCCQYYSY 120
Db 56 WYQKPGQAPRLIYGFSSRATGIPDRFGSGSGTDFTLTISRLPEDFAVYCCQYGS 115

Qy 121 PLTFGAGTKLELKRVTVAAPSVFIPPPSDEQLKSGTASVCLNNFYPREAKVQKVDNA 180
Db 116 QGTFGPGTKVDIKRTVAAPSVFIPPPSDEQLKSGTASVCLNNFYPREAKVQKVDNA 175

Qy 181 QSGNSQSVTEQDSKSTYLSSTLTLSKADYEHKHYACEVTHQGLSSPVTKSNRGE 240
Db 176 QSGNSQSVTEQDSKSTYLSSTLTLSKADYEHKHYACEVTHQGLSSPVTKSNRGE 235

RESULT 7
Q8TCD0 PRELIMINARY; PRT; 239 AA.
ID Q8TCD0
AC Q8TCD0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;

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RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Glandular pool- thyroid;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC022362; AAH2362.1; -.
DR PIR; S22658; S22658.
DR PIR; S34095; S34095.
DR PIR; S40324; S40324.
DR PIR; S40374; S40374.
DR PIR; S42267; S42267.
DR PIR; S42268; S42268.
DR HSSP; P01834; I17Z.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26234 MW; FACEDC3A3B03871D CRC64;

Query Match 78.6%; Score 976.5; DB 2; Length 239;
Best Local Similarity 80.2%; Pred. No. 3.2e-73;
Matches 190; Conservative 22; Mismatches 22; Indels 3; Gaps 2;

QY 5 AQLMLLLWVSGTCGDIYMSQSPDSLAVSLGERVTINCKSSQSLLYS-GNQKNYLAWQ 63
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
5 AQLGLLMLWPGSGDYVMTQSPLSLPTVLGQPASISCRSTQSLVYSDGN--TYLNNWFQ 62
QY 64 QKPGQSKLLIYWASARESGVDPDRFSGSGSGTDFLTITSSVQAEADVAVVYCOQYYSPLT 123
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
63 QKPGQSKLLIYKVNRSQVDPDRFSGSGSGTDFLTILTRVEADVGVYFCQGTHTWST 122
QY 124 FGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCILNLFYPREAKVQKVDNALQSG 183
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
123 FGQGTLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCILNLFYPREAKVQKVDNALQSG 182
QY 184 NSQSVTEQDSKDSITYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
183 NSQSVTEQDSKDSITYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 8
Q6P5S8 PRELIMINARY; PRT; 236 AA.
AC Q6P5S8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Glandular pool- thyroid;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Glandular pool- thyroid;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC062704; AAH62704.1; -.
DR HSSP; P01837; 1KCU.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25773 MW; 953E37BEB4FF5F27 CRC64;

Query Match 78.4%; Score 975; DB 2; Length 236;
Best Local Similarity 77.6%; Pred. No. 4.1e-73;
Matches 187; Conservative 29; Mismatches 19; Indels 6; Gaps 2;

QY 1 MDSQAQVLMILLWVSGTCGDIYMSQSPDSLAVSLGERVTINCKSSQSLLYSGNQKNYLA 60
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 METAQALLFLLLWLPDTTGEIVLTQSPGLTUSFSGERATILSCRSQTVFSS-----HLA 55
QY 61 WYQKPGQSKLLIYWASARESGVDPDRFSGSGSGTDFLTITSSVQAEADVAVVYCOQYYSY 120
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
56 WYQKPGQSKLLIYGASSRATGIPDRFSGSGSGTDFLTITRLEPEDFAVYFCQYQYGS 115
QY 121 P-LTFGAGTKLEKRTVAAPSVFIFPPSDEQLKSGTASVVCILNLFYPREAKVQKVDNA 179
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
116 PSLTFGGGTVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCILNLFYPREAKVQKVDNA 175
QY 180 LQSGNSQSVTEQDSKDSITYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGE 239
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
176 LQSGNSQSVTEQDSKDSITYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGE 235

240 C 240
236 C 236

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121 121 GPGTKVDIKRTVAAPSVPFIIPPDSDEQLKSGTASVVCLLNFFYPREAKQVQKVDNALQSGN 180
185 185 SQESVTQDSKSDSTYSLSLSTLTKADYERKHVYACVETVHQGLSSPPTKSFNRGEC 240
181 181 SQESVTQDSKSDSTYSLSLSTLTKADYERKHVYACVETVHQGLSSPPTKSFNRGEC 236

RESULT 10
Q6GMX8 PRELIMINARY; PRT; 236 AA.
AC Q6GMX8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073764; AAH73764.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; CI-set; 1.
DR SMART; SM00407; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559BFC9 CRC64;

Query Match 78.4%; Score 974; DB 2; Length 236;
Best Local Similarity 79.2%; Pred. No. 5e-73;
Matches 187; Conservative 23; Mismatches 20; Indels 6; Gaps 1;

Qy 5 AQLMLLLLVSGTCDIVMSQSPDSLAVSLGERTVTLNCKSSQSLLYSGNKVLAQQ 64
Db 7 AQLGLLLLVFPGRCDLQMTQSPSSVSASVGDRTVITCRASQGI-----SSMLVAQQ 60
Qy 65 KPGSPKLLIYWASARESGVDPDRFSGSGSGTDFTLTISVQAEDVAVVYCOQYYSYPLTF 124
Db 61 KPGKAPKLLIYAASSLQSGVSPDRFSGSGSGTDFTLTISLQPEDFATYCCQAHSFPPTF 120
Qy 125 GAGTKLEKRTVAAPSVPFIIPPDSDEQLKSGTASVVCLLNFFYPREAKQVQKVDNALQSGN 184
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Matches	187;	Conservative	19;	Mismatches	24;	Indels	6;	Gaps	1;
Qy	5	AQVLMILLVMSGTCGDIVMSQSPDSLAVSLGERVTLNCKSSQSLLSGNGKNYLAWYQQ	64						
Db	7	AQLGLILLLLWLRGARCIDIQMTQSPSSLASVSGDRAVITTCRASQ-----NINNYLNWYQL	60						
Qy	65	KPGOSPCLLLYWAARESGVDPDRSGSGSGCTDFTLTITSSVQAQADVAVVYCOQYYSYPLTF	124						
Db	61	KPGKAPNLLIYAASSLQSGVPSRFSGSGSGDFTLTITSSRPDPFATYVCOQSYNIPLTF	120						
Qy	125	GAGTKLELKTVAAPSFIIPPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN	184						
Db	121	GGGTINVEIKRTVAAPSFIIPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN	180						
Qy	185	SQSVTEQDSKDSYSLSSLTITLSKADYKHKVYACVETHQGLSSPYTKSFNRGEC	240						
Db	181	SQSVTEQDSKDSYSLSSLTITLSKADYKHKVYACVETHQGLSSPYTKSFNRGEC	236						

RESULT 13
723Y4 PRELIMINARY; PRT; 236 AA.
ID Q723Y4
AC Q723Y4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal Muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B.,onaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Munzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Goodman J., Green E.D., Dickson M.C.,
RA Krzywinski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Jonea S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RESULT 14
ID Q691
PRELIMINARY; PRT; 239 AA.
AC OGP491;
DT 05-JUL-2004 (TEMBLrel_27, Created)
DT 05-JUL-2004 (TEMBLrel_27, Last sequence update)
DT 05-JUL-2004 (TEMBLrel_27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo..
OX NCBI_TaxID=9606;
RN [1]
RP CSEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=23288257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler K.G.,
RA Altschul S.F., Zesberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.C., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Musny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
FAhey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.C., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RP	SEQUENCE FROM N.A.
RC	TISSUE=Skin;
RA	Strausberg R.;
RL	Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
RL	EMBL; BC063599; AAH63599.1; -.
DR	HSSP; P01837; 1KCU.
DR	InterPro; IPR003599; Ig.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003597; Ig.cl.
DR	InterPro; IPR003006; Ig.MHC.
DR	InterPro; IPR003596; Ig.v.
DR	Pfam; PF07654; Cl-set; 1.
DR	SMART; SM00409; Ig; 2.
DR	SMART; SM00407; Igcl; 1.
DR	SMART; SM00406; IgV; 1.

DR PROSITE; PS00835; IG LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 239 AA; 26245 MW; CD7313DDDFD358B3 CRC64;
 Query Match 77.2%; Score 959.5; DB 2; Length 239;
 Best Local Similarity 78.8%; Pred. No. 8.2e-72;
 Matches 186; Conservative 22; Mismatches 27; Indels 1; Gaps 1;
 Qy 5 AQLMLLLLVSGTCGDIVMSQSPDSLAVSLGERTVTLNCKSSQSLLYSGNOKNYLAWYQQ 64
 Db 5 AQLGLLLMLVPGSSGDIVMTQTLPSPTVLGQPASISCRSSSLLHS-NGNTYLSMLHQ 63
 Qy 65 KPGSPKLLIYWASARESGVDPDRFSGSGGTDFTLTITSSVQAEADVAVVYCOQYYSPLTF 124
 Db 64 RPGQPPRLIIYKISNRFSGVDPDRFSGSGAGTDFTLKISRVEADVGVYCMQVSHFPTF 123
 Qy 125 GAGTKLELKRIVTAAPSVFIIPPSPDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGN 184
 Db 124 GQGTVEIKRTVAAPSVFIIPPSPDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGN 183
 Qy 185 SQESVTEQDSKDYSLSSSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSNRGEC 240
 Db 184 SQESVTEQDSKDYSLSSSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSNRGEC 239

RESULT 15

Q6PIT5 ID Q6PIT5 PRELIMINARY; PRT; 236 AA.
 AC Q6PIT5; TISSUE=Lung;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 Krzywicki M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
 Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Strauberg R.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC029444; AAH29444.1; -.
 DR HSSP; P01607; 1AR2.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG-cl.
 DR InterPro; IPR003006; IG_MHC.

DR InterPro; IPR003596; IG v.
 DR Pfam; PF07654; Cl-set; 1.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGcl; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS00835; IG LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 236 AA; 25741 MW; BD50AP071FE3E351 CRC64;
 Query Match 77.1%; Score 958; DB 2; Length 236;
 Best Local Similarity 79.7%; Pred. No. 1.1e-71;
 Matches 188; Conservative 16; Mismatches 26; Indels 6; Gaps 1;
 Qy 5 AQLMLLLLVSGTCGDIVMSQSPDSLAVSLGERTVTLNCKSSQSLLYSGNOKNYLAWYQQ 64
 Db 7 AQLGLLLMLPGARCAIQLTQSPSSLSASVGERVTITCRASQGI-----SSALAWYQQ 60
 Qy 65 KPGSPKLLIYWASARESGVDPDRFSGSGGTDFTLTITSSVQAEADVAVVYCOQYYSPLTF 124
 Db 61 KPGPPKLLIYDASTMESGVPSRFSGSGGTHFTLTITSSVQAEADVAVVYCOQYYSPLTF 120
 Qy 125 GAGTKLELKRIVTAAPSVFIIPPSPDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGN 184
 Db 121 GQGTVEIKRTVAAPSVFIIPPSPDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGN 180
 Qy 185 SQESVTEQDSKDYSLSSSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSNRGEC 240
 Db 181 SQESVTEQDSKDYSLSSSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSNRGEC 236

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